

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:58:24 ; Search time 21 Seconds  
(without alignments)

114.514 Million cell updates/sec

Title: US-09-938-700-4

Perfect score: 136

Sequence: 1 CRVTHPLPKDIVRSIAKAPGKRAP 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 4988

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR\_78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	29	21.3	25	2	S07770	histone H2B.1, spe
2	28	20.6	11	2	S78765	ribosomal protein
3	27	19.9	16	2	PHI351	Ig heavy chain DJ
4	27	19.9	20	2	A41439	acid ribonuclease
5	27	19.9	25	1	ZJBP4	gene J protein - p
6	26.5	19.5	20	2	A36016	granulocyte inhibi
7	26.5	19.5	22	2	PQ0143	polygalacturonase
8	26	19.1	13	2	S32551	Glutathione transf
9	26	19.1	15	4	I38336	hypothetical TEL/M
10	26	19.1	20	2	JP0055	ribosomal protein
11	26	19.1	22	2	H30608	Ig kappa chain V-I
12	26	19.1	22	2	D30609	Ig kappa chain V-I
13	26	19.1	24	2	S30609	Ig kappa chain V-I
14	26	19.1	24	2	JP0052	ribosomal protein
15	25	18.4	10	2	H37196	bradykinin-potenti
16	25	18.4	15	2	PA0071	superoxide dismuta
17	25	18.4	15	2	I50503	agrin - electric r
18	25	18.4	17	2	D22595	bombolitin IV - Am
19	25	18.4	20	2	PS0028	flagellar motor sw
20	25	18.4	20	2	H28949	ribosomal protein
21	25	18.4	21	2	B33600	glutamate-ammonia
22	25	18.4	22	2	D47256	kinetoplast DNA-as
23	25	18.4	24	2	G85602	hypothetical prote
24	25	18.4	25	2	A60621	somatotropin - Atl
25	24	17.6	10	2	B37196	bradykinin-potenti
26	24	17.6	20	2	S23981	outer layer protei
27	24	17.6	20	2	S46479	retinoid-X-recepto
28	24	17.6	21	2	S51066	ribosomal protein
29	24	17.6	22	2	C42856	hypothetical prote

30 24 17.6 22 2 S42567 cytochrome-b5 redu  
31 23.5 17.3 23 2 PS0273 hypothetical prote  
32 23.5 17.3 23 2 A41263 kinase-related tra  
33 23 16.9 10 2 S77990 cytochrome-c oxida  
34 23 16.9 15 2 B39109 hypothetical 1-5K  
35 23 16.9 16 2 S65709 major allergen Myr  
36 23 16.9 16 2 PHI317 Ig heavy chain DJ  
37 23 16.9 18 2 B27504 histone H2B - mous  
38 23 16.9 19 2 PA0012 superoxide dismuta  
39 23 16.9 20 2 S09025 carboxylesterase (  
40 23 16.9 20 2 A42865 Ca2+/calmodulin-de  
41 23 16.9 21 2 S57568 T cell receptor V-  
42 23 16.9 22 2 C48186 ATPase R1 subunit  
43 23 16.9 23 2 S23518 stromelysin (EC 3.  
44 23 16.9 23 2 S72535 probable acr-2 reg  
45 22 16.2 7 2 A44428 platelet aggregati

#### ALIGNMENTS

##### RESULT 1

S07770  
histone H2B.1, sperm - sea urchin (Echinus esculentus) (fragment)  
C:Species: Echinus esculentus  
C:Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 23-Feb-1997  
C:Accession: S07770  
R: Hill, C.S.; Thomas, J.O.  
Eur J Biochem 187, 145-153, 1990  
A:Title: Core histone-DNA interactions in sea urchin sperm chromatin. The N-terminal ta  
A:Reference number: S07769; MUID:90126812; PMID:2238202  
A:Accession: S07770  
A:Molecule type: protein  
A:Residues: 1-25 <HIL>  
C:Superfamily: histone H2B  
C:Keywords: chromosomal protein; DNA binding; nucleosome core; nucleus

Query Match 21.3%; Score 29; DB 2; Length 25;

Best Local Similarity 62.5%; Pred. No. 1.3e+03;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 18 KAPGKRAP 25

DB 4 KSPTKRSP 11

##### RESULT 2

S78765  
ribosomal protein MRP-S24, mitochondrial - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

C:Accession: S78765

R: Graack, H.R.

submitted to the Protein Sequence Database, July 1999

A:Reference number: S78760

A:Accession: S78765

A:Molecule type: protein

A:Residues: 1-11 <GRA>

C:Keywords: mitochondrial

File-11/Product: ribosomal protein MRP-S24 (fragment) #status experimental <MAT>

Query Match 20.6%; Score 28; DB 2; Length 11;

Best Local Similarity 40.0%; Pred. No. 7.8e+02;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 HPPLPKDIVR 14

DB 2 HVDVFKDLTK 11

##### RESULT 3

PHI351  
Ig heavy chain DJ region (clone C100-109B) - human (fragment)

```
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1351
R;Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A;Reference number: PH1302; MUID:93094761; PMID:1460419
A;Accession: PH1351
A;Molecule type: DNA
A;Residues: 1-16 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match      19.9%; Score 27; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      16 IAKAPGKRAP 25
Db      7 IGSTPGAREP 16

RESULT 4
A41439
acid ribonuclease (EC 3.1.1.-) - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 21-Mar-1996
C;Accession: A41439
R;Ohgi, K.; Sando, A.; Takizawa, Y.; Irie, M.
J. Biochem. 103, 267-273, 1988
A;Title: Purification of acid ribonucleases from bovine spleen.
A;Reference number: A41439; MUID:88227899; PMID:3131316
A;Accession: A41439
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <OHG>
C;Keywords: hydrolase

Query Match      19.9%; Score 27; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      5 HPHPKDI 12
Db      9 HLYFPKDL 16

RESULT 5
ZJBPG4
gene J protein - phage G4
C;Species: phage G4
C;Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 28-Jul-2000
C;Accession: A04259
R;Godson, G.N.; Barrell, B.G.; Staden, R.; Fiddes, J.C.
Nature 276, 236-247, 1978
A;Title: Nucleotide sequence of bacteriophage G4 DNA.
A;Reference number: A93200; MUID:79053264; PMID:714153
A;Accession: A04259
A;Molecule type: DNA
A;Residues: 1-25 <GOD>
A;Cross-references: GB:J02454; GB:M10724; GB:M11404; GB:V00657; NID:g15931; PIDN:CAA2401
C;Comment: Gene J protein is one of the structural components of the bacteriophage coat.
C;Superfamily: phage phi-X174 gene J protein
C;Keywords: DNA binding

Query Match      19.9%; Score 27; DB 1; Length 25;
Best Local Similarity 43.8%; Pred. No. 2.5e+03;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy      8 LPKDIVRSIAKAPGKR 23
Db      1 MKKSIRRSRSGSKGAR 16

us-09-938-700-4.closed.xpr

RESULT 6
A36016
granulocyte inhibitory protein - human
C;Species: Homo sapiens (man)
C;Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 30-May-1997
C;Accession: A36016
R;Hoerl, W.H.; Haag-Weber, M.; Georgopoulos, A.; Block, L.H.
Proc. Natl. Acad. Sci. U.S.A. 87, 6353-6357, 1990
A;Title: Physicochemical characterization of a polypeptide present in uremic serum that
A;Reference number: A36016; MUID:90349614; PMID:2385596
A;Accession: A36016
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <HOE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match      19.5%; Score 26.5; DB 2; Length 20;
Best Local Similarity 36.8%; Pred. No. 2.3e+03;
Matches 7; Conservative 5; Mismatches 2; Indels 5; Gaps 1;

Qy      11 DIVR----SIKAPGKRA 24
Db      1 DIVMTSPGTLVSPGERA 19

RESULT 7
PQ0143
polygalacturonase (EC 3.2.1.15) P26 - evening primrose (fragment)
C;Species: Oenothera organensis (evening primrose)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 06-Dec-1996
C;Accession: PQ0143
R;Brown, S.M.; Crouch, M.L.
Plant Cell 2, 263-274, 1990
A;Title: Characterization of a gene family abundantly expressed in Oenothera organensis
A;Reference number: JQ0992; MUID:9305658; PMID:2152116
A;Accession: PQ0143
A;Molecule type: mRNA
A;Residues: 1-22 <BRO>
A;Experimental source: pollen
C;Comment: This protein is specifically translated in the pollens.
C;Comment: This protein functions by depolymerizing pectin in the cell walls of the pistil
y growing tube.
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match      19.5%; Score 26.5; DB 2; Length 22;
Best Local Similarity 38.1%; Pred. No. 2.6e+03;
Matches 8; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy      1 CRVTHPLPKDIVRSTAKAPG 21
Db      1 CTITNAQL-FDITKYGAKGDG 20

RESULT 8
S32551
glutathione transferase (EC 2.5.1.18) mu (isoform pI 6.4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 05-Jan-1996
C;Accession: S32551; S32550
R;Singhal, S.S.; Saxena, M.; Ahmad, H.; Awasthi, Y.C.
Biochim. Biophys. Acta 1116, 137-146, 1992
A;Title: Glutathione S-transferases of mouse liver: sex-related differences in the expression
A;Reference number: S32548; MUID:92256466; PMID:1581342
A;Accession: S32551
A;Molecule type: protein
A;Residues: 1-13 <SINI>
A;Experimental source: female
A;Accession: S32550
A;Molecule type: protein
A;Residues: 1-13 <SIN2>
A;Experimental source: male
C;Keywords: transferase
```

Query Match 19.1%; Score 26; DB 2; Length 13;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RVTHP 6  
 DB 9 RLTHP 13

RESULT 9  
 I38336  
 hypothetical TEL/MN1 mutant fusion protein type I - human (fragment)  
 C:Species: Homo sapiens (man)  
 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 20-Apr-2000  
 C;Accession: I38336  
 R;Buijs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.  
 Oncogene 10, 1511-1519, 1995  
 A;Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion of TEL and MN1 genes  
 A;Reference number: I38031; MUID:95249265; PMID:7731705  
 A;Accession: I38336  
 A;Status: translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-15 <BUI>  
 A;Cross-references: EMBL:X85026; NID:g971473; PIDN:CAA59399.1; PID:g971474  
 C;Comment: This sequence is the chimeric product of a translocation mutation.  
 C;Genetics:  
 A;Gene: ERV6/MN1; TEL/MN1  
 A;Map position: 22q11/12p13  
 C;Keywords: fusion protein

Query Match 19.1%; Score 26; DB 4; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 2.1e+03;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 HLPKDI 12  
 DB 6 HLPDHL 11

RESULT 10  
 JP0055  
 ribosomal protein L30 - Bacillus polymyxa (fragment)  
 C:Species: Bacillus polymyxa  
 C;Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 02-Sep-2000  
 C;Accession: JP0055  
 R;Ochi, K.  
 submitted to JIPID, February 1994  
 A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal protein L30  
 A;Reference number: JP0042  
 A;Accession: JP0055  
 A;Molecule type: protein  
 A;Residues: 1-20 <OCHI>  
 C;Superfamily: Escherichia coli ribosomal protein L30  
 C;Keywords: protein biosynthesis; ribosome

Query Match 19.1%; Score 26; DB 2; Length 20;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+03;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 IVRSLIAPG 21  
 DB 7 LVRSLIGRFG 16

RESULT 11  
 H30608  
 Ig kappa chain V-III region (Ste) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 30-May-1997  
 C;Accession: H30608  
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc  
 J. Immunol. 142, 3158-3163, 1989  
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies

A;Reference number: A30601; MUID:89215279; PMID:2496160  
 A;Accession: H30608  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-22 <GON>  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotrimer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 22;  
 Best Local Similarity 40.0%; Pred. No. 3e+03;  
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SIAPGKRA 24  
 DB 10 TLSVSPGERA 19

RESULT 12  
 D30609  
 IG kappa chain V-III regions (Jon and Mit) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 30-May-1997  
 C;Accession: D30609  
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc  
 J. Immunol. 142, 3158-3163, 1989  
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies  
 A;Reference number: A30601; MUID:89215279; PMID:2496160  
 A;Accession: D30609  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-22 <GON>  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotrimer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 22;  
 Best Local Similarity 40.0%; Pred. No. 3e+03;  
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SIAPGKRA 24  
 DB 10 TLSVSPGERA 19

RESULT 13  
 B30609  
 Ig kappa chain V-III region (She) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 30-May-1997  
 C;Accession: B30609  
 R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solc  
 J. Immunol. 142, 3158-3163, 1989  
 A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies  
 A;Reference number: A30601; MUID:89215279; PMID:2496160  
 A;Accession: B30609  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-24 <GON>  
 C;Superfamily: immunoglobulin V region; immunoglobulin homology  
 C;Keywords: heterotrimer; immunoglobulin

Query Match 19.1%; Score 26; DB 2; Length 24;  
 Best Local Similarity 40.0%; Pred. No. 3.3e+03;  
 Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SIAPGKRA 24  
 DB 10 TLSVSPGERA 19

RESULT 14  
 JP0052  
 ribosomal protein L30 - Bacillus macquariensis (fragment)  
 C:Species: Bacillus macquariensis

C;Date: 10-Mar-1994 #sequence\_revision 28-Oct-1994 #text\_change 02-Sep-2000  
C;Accession: JF0052  
R;Ochi, K.  
A;Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal p  
A;Reference number: JF0042  
A;Accession: JF0052  
A;Molecule type: protein  
A;Residues: 1-24 <OCH>  
C;Superfamily: Escherichia coli ribosomal protein L30  
C;Keywords: protein biosynthesis; ribosome

Query Match 19.1%; Score 26; DB 2; Length 24;  
Best Local Similarity 50.0%; Pred. No. 3.3e+03;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 12 IVRSIAKAPG 21  
DB 8 LVRSLLGRPG 17

RESULT 15  
H37196  
bradykinin-potentiating peptide 8 - island jararaca  
C;Species: Bothrops insularis (island jararaca)  
C;Date: 14-Feb-1992 #sequence\_revision 01-Dec-1992 #text\_change 05-Aug-1994  
C;Accession: H37196  
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.  
J. Protein Chem. 9, 221-227, 1990  
A;Title: Primary structure and biological activity of bradykinin potentiating peptides f  
A;Reference number: A37196; PMID:2386615  
A;Accession: H37196  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-10 <CIN>  
C;Keywords: pyroglutamic acid  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.4%; Score 25; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 1.9e+03;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 HPHLP 9  
DB 5 HFNIP 9

Search completed: March 18, 2004, 14:02:08  
Job time : 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:54:34 ; Search time 11 seconds  
(without alignments)  
118.341 Million cell updates/sec

Title: US-09-938-700-4

Perfect score: 136

Sequence: 1 CRVTHPLPKDIVRSIAKAPGKRAP 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 1653

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	22.8	18	1	CT1C_LITCI
2	29	21.3	18	1	CT1A_LITCI
3	29	21.3	25	1	H2B1_ECHES
4	27	19.9	12	1	PK4_PERAM
5	27	19.9	25	1	VG1_BEGA
6	26.5	19.5	19	1	TPP3_LEUMA
7	26	19.1	13	1	UP71_LITSEW
8	26	19.1	15	1	UC06_MAIZE
9	26	19.1	16	1	CT12_LITCI
10	26	19.1	18	1	CT1D_LITCI
11	25	18.4	10	1	BPP8_BOTIN
12	25	18.4	13	1	AU11_LITRA
13	25	18.4	13	1	AU12_LITRA
14	25	18.4	15	1	MCA2_RHOOP
15	25	18.4	16	1	CT13_LITCI
16	25	18.4	17	1	BOL4_MEGPE
17	25	18.4	19	1	TRPB_KLEAE
18	25	18.4	20	1	RUC1_HALMA
19	25	18.4	25	1	CR23_LITCE
20	25	18.4	25	1	CR24_LITCE
21	24	17.6	10	1	BPP2_BOTIN
22	24	17.6	15	1	MAOX_CHICK
23	24	17.6	16	1	AU22_LITAU
24	24	17.6	16	1	AU23_LITAU
25	24	17.6	16	1	CT11_LITCI
26	24	17.6	16	1	H5_COTJA
27	24	17.6	17	1	AU31_LITRA
28	24	17.6	17	1	AU32_LITRA
29	24	17.6	17	1	AU33_LITRA
30	24	17.6	18	1	CT1B_LITCI
31	24	17.6	20	1	VM02_CHICK
32	24	17.6	23	1	NIFD_ANASL
33	23	16.9	10	1	CX0X_THUOB

#### ALIGNMENTS

##### RESULT 1

CT1C\_LITCI  
ID CT1C\_LITCI STANDARD; PRT; 18 AA.  
AC P81844;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Citropin 1.2.4.  
OS Litoria citropa (Australian blue mountains tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=94770;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=99435977; PubMed=10504394;  
RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,  
RA Wallace J.C., Tyler M.J.;  
RT "Host defence peptides from the skin glands of the Australian blue mountains tree-frog Litoria citropa. Solution structure of the antibacterial peptide citropin 1.1.";  
RL Eur. J. Biochem. 265:627-637(1999).  
CC -!- SURCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Dorsal and submental skin glands.  
KW Amphibian defense peptide.  
SQ SEQUENCE 18 AA; 1814 MW; 500BF778DS15ABD7 CRC64;  
Query Match 22.8%; Score 31; DB 1; Length 18;  
Best Local Similarity 33.3%; Pred. No. 2.2e+02;  
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

##### Qy 11 DIVRSIAKAPGKRAP 25

Db 4 DIKKVASVVGGLASP 18

##### RESULT 2

CT1A\_LITCI  
ID CT1A\_LITCI STANDARD; PRT; 18 AA.  
AC P81838;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Citropin 1.1.3.  
OS Litoria citropa (Australian blue mountains tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=94770;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=99435977; PubMed=10504394;  
RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,  
RA Wallace J.C., Tyler M.J.;

```

RT "Host defence peptides from the skin glands of the Australian blue
RT mountain tree-frog Litoria citropa. Solution structure of the
RT antibacterial peptide citropin 1-11."
RL Eur. J. Biochem. 265:627-637(1999).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Dorsal and submental skin glands.
KW Amphibian defense peptide.
SQ SEQUENCE 18 AA; 1814 MW; 500BF778D51F98D7 CRC64;

Query Match 21.3%; Score 29; DB 1; Length 18;
Best Local Similarity 26.5%; Pred. No. 4.3e+02;
Matches 4; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 11 DIVRSIAKPKGRAP 25
Db 4 DVIKKVASVIGLASP 18

RESULT 3
H2B1_ECHES
ID H2B1_ECHES STANDARD; PRT; 25 AA.
AC P13281;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Histone H2B-1, sperm (fragment).
OS Echinus esculentus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoides; Euechinoides; Echinacea; Echinoida; Echinidae; Echinus.
OX NCBI_TaxID=7648;
RN [1]
RP SEQUENCE.
RX MEDLINE=90126812; PubMed=2298202;
RA Hill C.S., Thomas J.O.;
RT "Core histone-DNA interactions in sea urchin sperm chromatin. The N-
RT terminal tail of H2B interacts with linker DNA."
RL Eur. J. Biochem. 187:145-153(1990).
CC -!- SUBUNIT: The nucleosome is an octamer containing two molecules
CC each of H2A, H2B, H3 and H4. The octamer wraps approximately 146
CC bp of DNA.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the histone H2B family.
DR PIR; S07770; S07770.
DR InterPro; IPR000558; Histone H2B.
DR PROSITE; PS00357; HISTONE H2B; PARTIAL.
KW Nuclear protein; Chromosomal protein; Nucleosome core; DNA-binding;
KW Multigene family.
FT NON_TER 25
SQ SEQUENCE 25 AA; 2693 MW; 9842DD3D73A3A9EC CRC64;

Query Match 21.3%; Score 29; DB 1; Length 25;
Best Local Similarity 62.5%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 18 KAPKGRAP 25
Db 4 KSPTKRSP 11

RESULT 4
PPK4_PPRAM
ID PPK4_PPRAM STANDARD; PRT; 12 AA.
AC P82619;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-4 (Pep-PK-4) (YXPR-L-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]

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RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Retrocerebral complex;
RX MEDLINE=99212469; PubMed=10196736;
RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
RT "Differential distribution of pyrokinin-isoforms in cerebral and
RT abdominal neurohemal organs of the American cockroach."
RL Insect Biochem. Mol. Biol. 29:139-144(1999).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Ragana-specific distribution of FXPRlanides in the nervous system of
RT the American cockroach."
RL J. Comp. Neurol. 419:352-363(2000).
CC -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -!- TISSUE SPECIFICITY: Cordora cardiaca.
CC -!- MASS SPECTROMETRY: MW=1147.9; METHOD=MALDI.
CC -!- SIMILARITY: Belongs to the pyrokinin family.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 12
SQ SEQUENCE 12 AA; 1449 MW; FA7A3049FP42CAA1 CRC64;

Query Match 19.9%; Score 27; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 HLPKDI 12
Db 2 HLPKDV 7

RESULT 5
VGJ_BPG4
ID VGJ_BPG4 STANDARD; PRT; 25 AA.
AC P03652;
DT 21-JUN-1986 (Rel. 01, Created)
DT 21-JUN-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Small core protein (J protein).
GN J.
OS Bacteriophage G4.
OX Viruses; ssDNA viruses; Microviridae; Microvirus.
OX NCBI_TaxID=10843;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=79053264; PubMed=714153;
RA Godson G.N., Barrell B.G., Staden R., Fiddes J.C.;
RT "Nucleotide sequence of bacteriophage G4 DNA."
RL Nature 276:236-247(1978).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RX MEDLINE=96217890; PubMed=8642594;
RA McKenna R., Bowman B.R., Liag L.L., Rosemann M.G., Fane B.A.;
RT "Atomic structure of the degraded capsid particle of the
RT bacteriophage G4: induced structural changes in the presence of
RT calcium ions and functional implications."
RL J. Mol. Biol. 256:736-750(1996).
CC -!- FUNCTION: The J protein is associated with the DNA and is situated
CC in an interior cleft of the F protein.
CC -!- SUBUNIT: The virion is composed of 60 copies each of the F, G, and
CC J proteins, and 12 copies of the H protein.
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EMBL; V00657; CAA24018.1; --
PIR; A04259; ZJBPG4.

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PDB; 1GFF; 03-APR-96.
InterPro; IPR006815; Microvir_J.
Pfam; PF04726; Microvir_J; 1.
Coat protein; DNA-binding; 3D-structure.
SEQUENCE 25 AA; 2815 MW; 87B7A8DFFFDD033 CRC64;

Query Match          19.9%; Score 27; DB 1; Length 25;
Best Local Similarity 43.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY      8 LPKDIVRSIAKPGKR 23
       :|:|||||:|
Db      1 MKKSIRSGGSKGAR 16

RESULT 6
TRP3 LEUMA STANDARD; PRT; 19 AA.
ID TRP3 LEUMA
AC P81735;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tachykinin-related peptide 3 (LemTRP 3).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RC SEQUENCE.
RP TISSUE=Midgut;
RX MEDLINE=97053012; PubMed=8897641;
RA Muren J.E., Naessel D.R.;
RT "Isolation of five tachykinin-related peptides from the midgut of
   the cockroach Leucophaea maderae: existence of N-terminally extended
   isoforms.";
RL Regul. Pept. 65:185-196(1996);
CC -|- FUNCTION: Myoactive peptide. Increases the amplitude and frequency
   of spontaneous contractions and tonus of hindgut muscle.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Midgut.
CC -|- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 19
SQ SEQUENCE 19 AA; 1930 MW; 99B5471A011625E5 CRC64;

Query Match          19.5%; Score 26.5; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY      18 KAPG-KRAP 25
       :|||:|
Db      4 RAPGSKAP 12

RESULT 7
UP71 LITEW STANDARD; PRT; 13 AA.
ID UP71 LITEW
AC P82050;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uperin 7.1 [Contains: Uperin 7.1.1].
OS Litorea ewingi (Brown tree frog) (Ewing's tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylloidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104896;
RN [1]
RC SEQUENCE, AND MASS SPECTROMETRY.
RP TISSUE=Skin secretion;
RA Steinborner S.T., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "An unusual combination of peptides from the skin glands of Ewing's
```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 [1]  
 RN SEQUENCE.  
 RP TISSUE=Skin secretion;  
 RC MEDLINE=99435977; PubMed=10504394;  
 RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,  
 RA Wallace J.C., Tyler M.J.;  
 RT "Host defence peptides from the skin glands of the Australian blue  
 RT mountains tree-frog Litoria citropa. Solution structure of the  
 RT antibacterial peptide citropin 1.1.";  
 RL Eur. J. Biochem. 265:627-637(1999).  
 CC -!- FUNCTION: Bacteriostatic action for Gram-positive bacteria.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC Amphibian defense peptide; Antibiotic; Amidation.  
 KW PEPTIDE 1 16  
 FT CITROPIN 1.2.  
 FT PEPTIDE 3 14  
 FT CITROPIN 1.2.1.  
 FT PEPTIDE 4 14  
 FT CITROPIN 1.2.2.  
 FT PEPTIDE 1 11  
 FT CITROPIN 1.2.3.  
 FT MOD RES 16 16  
 AMIDATION.  
 SQ SEQUENCE 16 AA; 1616 MW; 1D878515ABD73DE9 CRC64;  
 Query Match 19.1%; Score 26; DB 1; Length 16;  
 Best Local Similarity 36.4%; Pred. No. 1e+03;  
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 11 DIVRSIAKAPG 21  
 ||:|:  
 Db 4 DIKKVASVWG 14

RESULT 10  
 CTID LITCI STANDARD; PRT; 18 AA.  
 AC P81845;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Citropin 1.2.5.  
 OS Litoria citropa (Australian blue mountains tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=94770;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=99435977; PubMed=10504394;  
 RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,  
 RA Wallace J.C., Tyler M.J.;  
 RT "Host defence peptides from the skin glands of the Australian blue  
 RT mountains tree-frog Litoria citropa. Solution structure of the  
 RT antibacterial peptide citropin 1.1.";  
 RL Eur. J. Biochem. 265:627-637(1999).  
 CC -!- TISSUE SPECIFICITY: Dorsal and submental skin glands.  
 KW Amphibian defense peptide.  
 SQ SEQUENCE 18 AA; 1845 MW; 51BBF778D515ABD7 CRC64;  
 Query Match 19.1%; Score 26; DB 1; Length 18;  
 Best Local Similarity 36.4%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 11 DIVRSIAKAPG 21  
 ||:|:  
 Db 4 DIKKVASVWG 14

RESULT 11  
 BPP8 BOTIN  
 ID BPP8\_BOTIN STANDARD; PRT; 10 AA.

P30426;  
 AC 01-APR-1993 (Rel. 25, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Bradykinin-potentiating peptide S5.1 (Angiotensin-converting  
 DE enzyme inhibitor).  
 OS Bothrops insularis (Iland jararaca) (Queimada jararaca).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Bothrops.  
 OX NCBI\_TaxID=8723;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=90351557; PubMed=2386615;  
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;  
 RT "Primary structure and biological activity of bradykinin potentiating  
 RT peptides from Bothrops insularis snake venom.";  
 RL J. Protein Chem. 9:221-227(1990).  
 CC -!- FUNCTION: This peptide both inhibits the activity of the  
 CC angiotensin-converting enzyme and enhances the action of  
 CC bradykinin by inhibiting the kinases that inactivate it.  
 CC It acts as an indirect hypotensive agent.  
 DR PIR; H37196; H37196.  
 KW Hypotensive agent; Pyrrolidone carboxylic acid.  
 FT MOD RES 1 1  
 PYRROLIDONE CARBOXYLIC ACID.  
 SQ SEQUENCE 10 AA; 1173 MW; 2FF83545761F6D8 CRC64;  
 Query Match 18.4%; Score 25; DB 1; Length 10;  
 Best Local Similarity 60.0%; Pred. No. 9e+02;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 Qy 5 HPHLP 9  
 ||:|:  
 Db 5 HENIP 9

RESULT 12  
 AU11 LITRA STANDARD; PRT; 13 AA.  
 AC P82386;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Aurein 1.1.  
 OS Litoria raniformis (Southern bell frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=116057;  
 RN [1]  
 RP SEQUENCE, AND FUNCTION.  
 RC TISSUE=Skin secretion;  
 RX MEDLINE=20408845; PubMed=10951191;  
 RA Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,  
 RA Wallace J.C., Tyler M.J.;  
 RT "The antibiotic and anticancer active aurein peptides from the  
 RT Australian bell frogs Litoria aurea and Litoria raniformis the  
 RT solution structure of aurein 1.2.";  
 RL Eur. J. Biochem. 267:5330-5341(2000).  
 CC -!- FUNCTION: Antimicrobial activity against B.cereus, L.lactis,  
 CC Limococcus and S.suberis. Probably acts by disturbing membrane  
 CC functions with its amphipathic structure.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 KW Amphibian defense peptide; Antibiotic; Amidation.  
 FT MOD RES 13 13  
 AMIDATION.  
 SQ SEQUENCE 13 AA; 1447 MW; 173CB99DF8C83330 CRC64;

Query Match 18.4%; Score 25; DB 1; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 1.2e+03;  
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;



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QY 11 DIVRSIAXA 19
DB 4 DIIKXIAES 12

RESULT 13
AUI2_LITRA STANDARD; PRT; 13 AA.
ID AUI2_LITRA
AC P82387;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aurein 1.2.
OS Litoria raniformis (Southern bell frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=116057;
RN [1]
RP SEQUENCE, FUNCTION, AND STRUCTURE BY NMR.
RC TISSUE=Skin secretion;
RX MEDLINE=20408845; PubMed=10951191;
RA Rozek T., Wegener K.L., Bowie J.H., Olver I.N., Carver J.A.,
RA Wallace J.C., Tyler M.J.;
RT "The antibiotic and anticancer active aurein peptides from the
RT Australian bell frogs Litoria aurea and Litoria raniformis the
RT solution structure of aurein 1.2."
RL Eur. J. Biochem. 267:5330-5341(2000).
CC L.innocua, M.luteus, P.multocida, S.aureus, S.epidermidis and
CC S.uberis. Probably acts by disturbing membrane functions with its
CC amphipathic structure. Shows anticancer activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- TISSUE SPECIFICITY: Dorsal and submental skin glands.
KW Amphibian defense peptide; Amidation; Antibiotic.
FT MOD RES 13
FT SEQUENCE 13 AA; 1481 MW; 1EACB99DFBC83330 CRC64;
SQ
Query Match 18.4%; Score 25; DB 1; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 11 DIVRSIAXA 19
DB 4 DIIKXIAES 12

RESULT 14
MCA2_RHOOP STANDARD; PRT; 15 AA.
ID MCA2_RHOOP
AC P56870;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative maleylacetate reductase II (EC 1.3.1.32) (Fragment).
OS Rhodococcus opacus (Nocardia opaca).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardia; Rhodococcus.
OX NCBI_TaxID=37919;
RN [1]
RP SEQUENCE.
RC STRAIN=1CP;
RX MEDLINE=98324954; PubMed=9657989;
RA Seibert V., Kourbatova E.M., Golovleva L.A., Schloemann M.;
RT "Characterization of a maleylacetate reductase encoding region from
RT Rhodococcus opacus 1CP."
RL J. Bacteriol. 180:3503-3508(1998).
CC -1- CATALYTIC ACTIVITY: 3-oxoadipate + NAD(P)(+) = 2-maleylacetate +
CC NAD(P)H.
CC -1- PATHWAY: 3-chlorocatechol degradation (beta-ketoadipate pathway).
CC THIS PATHWAY SERVES A VITAL ROLE IN THE BIODEGRADATION OF TOXIC
CC AROMATIC COMPOUNDS INTRODUCED IN THE ENVIRONMENT BOTH AS NATURAL
CC PRODUCTS AND AS INDUSTRIAL EFFLUENT.
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CC -1- SIMILARITY: Belongs to the iron-containing alcohol dehydrogenase
CC family.
DR InterPro; IPR001670; Fe-ADH.
DR PROSITE; PS00913; ADH_IRON_1; PARTIAL.
DR PROSITE; PS00860; ADH_IRON_2; PARTIAL.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NAD.
FT NON TER 15
FT SEQUENCE 15 AA; 1884 MW; 58DA90DD038F025E CRC64;
SQ
Query Match 18.4%; Score 25; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDI 12
DB 2 RFEHENLPQRI 12

RESULT 15
CT13_LITCI STANDARD; PRT; 16 AA.
ID CT13_LITCI
AC P81846;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Citropin 1.3.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=99435977; PubMed=10504394;
RA Wegener K.L., Wabnitz P.A., Carver J.A., Bowie J.H., Chia B.C.S.,
RA Wallace J.C., Tyler M.J.;
RT "Host defence peptides from the skin glands of the Australian blue
RT mountains tree-frog Litoria citropa. Solution structure of the
RT antibacterial peptide citropin 1.1."
RL Eur. J. Biochem. 265:627-637(1999).
CC -1- FUNCTION: Bacteriostatic action for Gram-positive bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Dorsal and submental skin glands.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT MOD RES 16
FT SEQUENCE 16 AA; 1630 MW; 1D8785073BD73DE9 CRC64;
SQ
Query Match 18.4%; Score 25; DB 1; Length 16;
Best Local Similarity 36.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 11 DIVRSIAXAPG 21
DB 4 DIIKVASVIG 14

Search completed: March 18, 2004, 14:00:44
Job time : 12 secs
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:57:54 ; Search time 38 Seconds  
(without alignments)  
207.578 Million cell updates/sec

Title: US-09-938-700-4  
Perfect score: 136  
Sequence: 1 CRVTHPLPKDIVRSIAKAPGRAP 25

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 11070

Minimum DB seq length: 0  
Maximum DB seq length: 25

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL 25:\*

```

1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	22.1	18	4 Q9BQT0	Q9bqt0 homo sapien
2	30	22.1	19	15 Q90RH8	Q90rh8 human immu
3	30	22.1	20	11 Q99JV2	Q99jv2 mus musculu
4	29	21.3	16	8 Q9T2R0	Q9t2r0 solanum tub
5	29	21.3	19	4 Q16271	Q16271 homo sapien
6	28	20.6	22	7 Q9MX47	Q9mx47 oryzias lat
7	28	20.6	24	2 Q9L7N8	Q9l7n8 borrelia af
8	27	19.9	15	4 Q9UEM3	Q9uem3 homo sapien
9	27	19.9	20	4 Q9UM18	Q9um18 homo sapien
10	27	19.9	21	6 Q9NCJ5	Q9ncj5 saguinus im
11	27	19.9	24	10 Q7XAX3	Q7xax3 brassica ra
12	26.5	19.5	17	5 Q9TWR3	Q9twr3 trypanosoma
13	26.5	19.5	22	10 Q9S9B8	Q9s9b8 oenothera o
14	26	19.1	15	4 Q9UCJ8	Q9ucj8 homo sapien
15	26	19.1	16	8 Q9T2V8	Q9t2v8 homo sapien
16	26	19.1	18	6 Q95JA2	Q95ja2 sus scrofa

17	19.1	26	21	12	Q85667	Q85667 reovirus (c
18	19.1	26	24	2	Q9L7N6	Q9l7n6 borrelia bi
19	19.1	26	25	11	Q9QUW9	Q9quw9 rattus sp.
20	18.8	25.5	16	6	Q9TRD1	Q9trd1 sus scrofa
21	18.8	25.5	24	5	Q9U542	Q9u542 aedes agasp
22	18.4	25	13	2	Q8GBU2	Q8gbu2 vibrio harv
23	18.4	25	14	3	P90342	P90342 saccharomyc
24	18.4	25	15	13	Q90403	Q90403 discopyge o
25	18.4	25	17	6	Q9XSG1	Q9xsg1 bos taurus
26	18.4	25	18	2	Q9RAE0	Q9rae0 pseudomonas
27	18.4	25	19	13	Q42416	Q42416 gallus gall
28	18.4	25	19	15	Q90RH4	Q90rh4 human immu
29	18.4	25	21	4	Q9H4Z8	Q9h4z8 homo sapien
30	18.4	25	22	5	Q9TWU8	Q9twu8 crithidia f
31	18.4	25	22	13	Q9PS65	Q9ps65 oncorhynch
32	18.4	25	23	2	Q43887	Q43887 anabaena az
33	18.4	25	23	5	Q95S95	Q95s95 drosophila
34	18.4	25	23	10	Q94IS9	Q94is9 pinus taeda
35	18.4	25	24	2	Q9KIL6	Q9kil6 streptomyce
36	18.4	25	24	16	Q8XAG7	Q8xag7 escherichia
37	18.4	25	25	10	Q94IS2	Q94is2 pinus radia
38	18.4	25	25	12	Q80J46	Q80j46 cyster noro
39	18.4	25	25	12	Q80J44	Q80j44 oyster noro
40	18.4	25	25	12	Q80J43	Q80j43 oyster noro
41	18.0	24.5	20	13	Q9PSH5	Q9psH5 gallus gall
42	18.0	24.5	25	6	Q8MI11	Q8mi11 bos taurus
43	17.6	24	13	8	Q33417	Q33417 digitalis p
44	17.6	24	15	11	Q9QV01	Q9qv01 mus sp. 16
45	17.6	24	17	2	Q34216	Q34216 sphingomona

## ALIGNMENTS

## RESULT 1

```

Q9BQT0 ID Q9BQT0 PRELIMINARY; PRT; 18 AA.
AC Q9BQT0;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21195339; PubMed=11297743;
RA Holzmann K., Ambrosch I., Elbling L., Micksche M., Berger W.;
RT "A small upstream open reading frame causes inhibition of human major
RT vault protein expression from a ubiquitous mRNA splice variant.";
RL FEBS Lett. 494:99-104(2001).
DR EMBL; AJ291367; CAC35315.1; -.
KW Hypothetical protein.
SQ SEQUENCE 18 AA; 2179 MW; 5D06F9A3F11CB828 CRC64;

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Query Match 22.1%; Score 30; DB 4; Length 18;  
Best Local Similarity 66.7%; Pred. No. 1.8e+03;  
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 CRVTHPLP 9  
|||  
Db 8 CRL--PHLP 14

## RESULT 2

```

Q90RH8 ID Q90RH8 PRELIMINARY; PRT; 19 AA.
AC Q90RH8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)

```

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DE Tat protein (Fragment).
GN TAT.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=96CG12;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
RA Hayami M., Ichimura H., Parra J.H.;
RT "Genetic Subtypes of HIV Type 1 Based on the vpu/env Sequences in
RL Republic of Congo-Brazzaville.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF127545; AAK84896.1; -
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2210 MW; 2A83642B89068236 CRC64;

Query Match 22.1%; Score 30; DB 15; Length 19;
Best Local Similarity 53.8%; Pred. No. 1.9e+03;
Matches 7; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 PHLPKDIVRSIAK 18
Db 7 PHSSKDHQNSIPK 19

RESULT 3
Q99JV2 PRELIMINARY; PRT; 20 AA.
AC Q99JV2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005653; AAH05653.1; -
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2223 MW; F203F6A80A7A0429 CRC64;

Query Match 22.1%; Score 30; DB 11; Length 20;
Best Local Similarity 70.0%; Pred. No. 2e+03;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 13 VRSIAKAPGK 22
Db 1 VFSAAKRPCK 10

RESULT 4
Q9T2R0 PRELIMINARY; PRT; 16 AA.
AC Q9T2R0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytochrome-C reductase 14 kDa subunit (EC 1.10.2.2) (Fragment).
OS Solanum tuberosum (Potato).
OG Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
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RP SEQUENCE.
RX MEDLINE=94198758; PubMed=7764624;
RA Braun H.P., Kruft V., Schmitz U.K.;
RL Planta 193:99-106(1994).
DR GO: GO:0008121; F:ubiquinol-cytochrome-c reductase activity; IEA.
SQ SEQUENCE 16 AA; 1946 MW; B8C625F8E4A4C8E7 CRC64;

Query Match 21.3%; Score 29; DB 8; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 HPPLPKDIXI 12
Db 2 HQYLPEDL 9

RESULT 5
Q16271 PRELIMINARY; PRT; 19 AA.
AC Q16271;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Arginine vasopressin V2 receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Holtzman E.J., Kolakowski L.F.Jr., Geifman-Holtzman O., O'Brien D.G.,
RA Rasoulpour M., Guillot A.P., Ausiello D.A.;
RT "Mutations in the vasopressin V2 receptor gene in two families with
RT nephrogenic diabetes insipidus.";
RL J. Am. Soc. Nephrol. 5:169-176(1994).
DR EMBL: S75754; AAB32753.1; -
KW Receptor.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 1905 MW; 181640EFD90F2788 CRC64;

Query Match 21.3%; Score 29; DB 4; Length 19;
Best Local Similarity 37.5%; Pred. No. 2.7e+03;
Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

Qy 5 HPPLPKDIVRSIAKAP 20
Db 4 HPSLPSCAWASLSAQP 19

RESULT 6
Q9MX47 PRELIMINARY; PRT; 22 AA.
AC Q9MX47;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MHC class II antigen (Fragment).
GN ORLA-DCB.
OS Oryzias latipes (Medaka fish) (Japanese ricefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX NCBI_TaxID=8090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PHNI;
RA Naruse K., Oku H., Kojima A., Bessho Y., Kuroda N., Matsuzaki T.,
RA Hori H., Shima A., Nonaka M.;
RT "Molecular cloning and linkage analysis of medaka fish MHC class II B
RT genes.";
```

RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.  
DR  
DR EMBL: AB033216; BAA94283.1; -.  
DR InterPro: IPR007110; Ig-like.  
FT non\_ter 1  
FT non\_ter 1  
FT non\_ter 22  
FT non\_ter 22  
SQ SEQUENCE 22 AA: 2441 MW: E2AFIA9CD581F5FB CRC64;

Query Match 20.6%; Score 28; DB 7; Length 22;  
Best Local Similarity 38.5%; Pred. No. 4.4e+03;  
Matches 5; Conservative 2; Mismatches 6; Indels

Qy 1 CRVTHPHLPKDIV 13  
||| |  
Db 7 CRVEHVSLLKDEPLI 19  
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RESULT	7
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AC	Q9L7N8;
AD	01-OCT-2000 (TREMBlurel. 15, Created)
DT	01-OCT-2000 (TREMBlurel. 15, Last sequence update)
DT	01-OCT-2000 (TREMBlurel. 15, Last annotation update)
DE	Bmpd (Fragment).
GN	BMPD.
OS	Borrelia afzelii.
OC	Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX	(1)
RX	SEQUENCE FROM N.A.
RC	STRAIN=Ip3;
RX	MEDLINE=20179823; PubMed=10715014;
RA	Gorbacheva V.Y., Godfrey H.P., Cabello F.C.;
RT	"Analysis of the bmp gene family in Borrelia burgdorferi sensu lato"
RL	J. Bacteriol. 182:2037-2042(2000).
RD	EMBL; AF222435; AAF45174.1; --.
FT	NON TER 1
SF	SEQUENCE 24 AA; 2681 MW; 57F3887CD59126F9 CRC64;
SD	

Query Match 20.6%; Score 28; DB 2; Length 24;  
Best Local Similarity 46.2%; Pred. No. 4.9e+03;  
Matches 6; Conservative 2; Mismatches 5; Indels

Qy	12	IVRSIAKAPGKRA	24
		: : : :	
Dp	1	IINGIIKAPYDKA	13

RESULT 8		
ID	Q9UEM3	PRELIMINARY; PRT; 15 AA.
AC	Q9UEM3;	
DT	01-MAY-2000 (TEMBLrel. 13, Created)	
DT	01-MAY-2000 (T-EMBLrel. 13, Last sequence update)	
DT	01-MAY-2000 (T-EMBLrel. 13, Last annotation update)	
DE	Axonemal dynein, heavy chain (Fragment).	
GN	DNAB3.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	Matti A.K., Mattei M.G., Jorissen M., Volz A., Ziegler A.,	
RA	Bouvagnet P.	
RT	"Chromosomal localization of human dynein heavy chain genes."	
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.	
FR	EMBL; AJ132092; CAA10565.1; -.	
FT	NON TER 1	
FT	NON TER 1	
FT	NON TER 15	
SO	SEQUENCE 15 AA: 1646 MW: 4EDFDA937C826170 C064	

Query Match 19.9%; Score 27; DB 4; Length 15;

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Best Local Similarity 44.4%; Pred. No. 4.2e+03;
Matches      4; Conservative    4; Mismatches   1; Indels       0; Gaps         0;
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Qy          10 KDIVRSIAK 18  
||: ||:  
ob          6 KOLAKALAIK 14
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RESULT 9	Q9UM18	Q9UM18	PRELIMINARY;	PRT;	20 AA.
ID	Q9UM18	Q9UM18	PRELIMINARY;	PRT;	20 AA.
AC	Q9UM18;	Q9UM18	PRELIMINARY;	PRT;	20 AA.
DT	01-MAY-2000	(TrEMBLrel. 13, Created)			
DT	01-MAY-2000	(TrEMBLrel. 13, Last sequence update)			
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)			
DE	Mucin (Fragment)				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=892315154; PubMed=2715633;				
RA	Xing P.X., Tjandra J.J., Reynolds K., McLaughlin P.J., Purcell D.				
RA	McKenzie I.F.C.;				
RT	Reactivity of anti-human milk fat globule antibodies with synthe				
RT	peptides.";				
RL	J Immunol. 142:3503-3509(1989).				
DR	EMBL, M26316; AAA36336.1; -.				
DR	PIR; S10571; S10571.				
DR	NON TER 1				
FT	NON TER 20				
FT	NON TER 20				
SC	SEQUENCE 20 AA, 1887 MW: 5B3473EAEBAFAD87 CRC64;				

Query Match	19.9%;	Score 27;	DB 4;	Length 20;
Best Local Similarity	71.4%;	Pred. No. 5.7e+03;		

Qy 19 APGKRAP 25  
|||  
Db 6 APGSTAP 12

RESULT	10
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AC	Q9N0J5;
DT	01-OCT-2000 (TEMBLrel. 15, Created)
DT	01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT	01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE	Choline acetyltransferase (Fragment).
GN	CHAT.
OS	Saguinus imperator (Emperor tamarin), Saguinus olerosus (Common marmoset); Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euarchontoglires OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus
OX	NCB1_TaxID=9491;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Mumbilla M.V.;
RT	"CHAT gene evolution in the mammalian genome.";
RL	Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; AJ276478; CAB77548.1; -.
DG	GO; GO:0016740; F:transferase activity; IEA. KW Transferase.
KW	
FT	NON TER
SO	SEQUENCE 21 AA; 21
ST	CBS00293BC3B05AF CRC64;

Query Match 19.9%; Score 27; DB 6; Length 21;  
Best Local Similarity 46.7%; Pred. No. 5.9e+03;  
Matches 1. Mismatches 7; Indels

QY 6 PHLPKDIVRSIAKAP 20



RL Biochem. Soc. Trans. 22:427-431(1994).  
 DR GO:0005739; C-mitochondrion; NAS.  
 DR GO:0004300; F-acyl-CoA hydratase activity; NAS.  
 DR GO:0006835; P-fatty acid beta-oxidation; NAS.  
 SQ SEQUENCE 16 AA; 1763 MW; 31AD66A3080B019A CRC64;  
 Query Match 19.1%; Score 26; DB 8; Length 16;  
 Best Local Similarity 31.2%; Pred. No. 6.3e+03;  
 Matches 5; Conservative 3; Mismatches 8; Indels 0; Gaps 0;  
 Qy 10 KDIVRSIAKAPGRAP 25  
 Db 1 KPNIRNVVVVDGVRTP 16

Search completed: March 18, 2004, 14:01:36  
 Job time : 40 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2004, 14:01:40 ; Search time 39 Seconds  
(without alignments)

165.997 Million cell updates/sec

Title: US-09-938-700-4

Perfect score: 136

Sequence: 1 CRVTHPLPKDIVRSIAKAPGKRAP 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 214167

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
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15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	136	100.0	25	9	US-09-938-700-4
2	89	65.4	17	15	US-10-325-375A-2
3	72	52.9	17	15	US-10-325-375A-4
4	69	50.7	17	15	US-10-325-375A-3
5	65	47.8	17	15	US-10-325-375A-6
6	61	44.9	17	15	US-10-325-375A-5
7	60	44.1	14	12	US-10-362-527-313
8	60	44.1	14	14	US-10-304-443-107
9	60	44.1	16	14	US-10-304-443-97
10	60	44.1	16	14	US-10-304-443-120
11	60	44.1	18	12	US-10-362-527-315
12	60	44.1	18	12	US-10-362-527-321
13	60	44.1	18	14	US-10-304-443-98
14	60	44.1	18	14	US-10-304-443-109
15	60	44.1	18	14	US-10-304-443-115

16	60	44.1	18	14	US-10-304-443-121	Sequence 121, App
17	60	44.1	20	12	US-10-362-527-316	Sequence 316, App
18	60	44.1	20	12	US-10-362-527-322	Sequence 322, App
19	60	44.1	20	14	US-10-304-443-110	Sequence 110, App
20	60	44.1	20	14	US-10-304-443-116	Sequence 116, App
21	60	44.1	25	9	US-09-974-449-33	Sequence 33, Appl
22	56	41.2	14	14	US-10-304-443-96	Sequence 96, Appl
23	56	41.2	14	14	US-10-304-443-119	Sequence 119, Appl
24	56	41.2	16	12	US-10-362-527-314	Sequence 314, App
25	56	41.2	16	12	US-10-362-527-320	Sequence 320, App
26	56	41.2	16	14	US-10-362-527-108	Sequence 108, App
27	56	41.2	16	14	US-10-304-443-114	Sequence 114, App
28	55	40.4	19	12	US-10-362-527-62	Sequence 62, Appl
29	55	40.4	19	14	US-10-322-210-3	Sequence 3, Appli
30	55	40.4	19	14	US-10-304-443-3	Sequence 3, Appli
31	51	37.5	12	14	US-10-304-443-95	Sequence 95, Appl
32	51	37.5	13	12	US-10-362-527-77	Sequence 77, Appl
33	51	37.5	13	14	US-10-322-210-18	Sequence 18, Appl
34	51	37.5	13	14	US-10-304-443-18	Sequence 94, Appl
35	45	33.1	10	14	US-10-304-443-94	Sequence 312, App
36	45	33.1	12	12	US-10-362-527-312	Sequence 106, App
37	45	33.1	12	14	US-10-304-443-106	Sequence 43303, A
38	44	32.4	20	9	US-09-864-761-43303	Sequence 76, Appl
39	42	30.9	12	12	US-10-362-527-76	Sequence 17, Appl
40	42	30.9	12	14	US-10-322-210-17	Sequence 17, Appl
41	42	30.9	12	14	US-10-304-443-17	Sequence 8, Appli
42	42	30.9	16	15	US-10-325-375A-8	Sequence 93, Appl
43	41	30.1	8	14	US-10-304-443-93	Sequence 311, App
44	41	30.1	10	12	US-10-362-527-311	Sequence 105, App
45	41	30.1	10	14	US-10-304-443-105	

#### ALIGNMENTS

RESULT 1  
US-09-938-700-4  
; Sequence 4, Application US/09938700  
; Patent No. US20020064525A1  
; GENERAL INFORMATION:  
; APPLICANT: Morsey, et al.  
; TITLE OF INVENTION: Anti-IgE Vaccines  
; FILE REFERENCE: PC10761A  
; CURRENT APPLICATION NUMBER: US/09/938,700  
; CURRENT FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 25  
; TYPE: PRT  
; ORGANISM: DOG CH3/CH4 PEPTIDE SEQUENCE  
US-09-938-700-4

Query Match 100.0%; Score 136; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e-12;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRVTHPLPKDIVRSIAKAPGKRAP 25  
Db 1 CRVTHPLPKDIVRSIAKAPGKRAP 25

RESULT 2  
US-10-325-375A-2  
; Sequence 2, Application US/10325375A  
; Publication No. US20030229021A1  
; GENERAL INFORMATION:  
; APPLICANT: IDEXX Laboratories, Inc.  
; APPLICANT: Krah, Eugene R.  
; APPLICANT: Lawton, Robert  
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of IgE to a High  
; TITLE OF INVENTION: Affinity Receptor  
; FILE REFERENCE: MBHB-01-672-E

```
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to IgE.
US-10-325-375A-2

Query Match          65.4%; Score 89; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 6.3e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSI 16
   |||||:|||||
Db 2 CRVTHPLPKDIVRSI 17

RESULT 3
US-10-325-375A-4
; Sequence 4, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krah, Eugene R.
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of IgE to a High
; TITLE OF INVENTION: Affinity Receptor
; FILE REFERENCE: MBHB-01-672-E
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to IgE.
US-10-325-375A-4

Query Match          52.9%; Score 72; DB 15; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.0017;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSI 15
   |||||:|||||
Db 2 CRVTHPLPKDIVRSI 16

RESULT 4
US-10-325-375A-3
; Sequence 3, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krah, Eugene R.
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of IgE to a High
; TITLE OF INVENTION: Affinity Receptor
; FILE REFERENCE: MBHB-01-672-E
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to IgE.
US-10-325-375A-3

Query Match          50.7%; Score 69; DB 15; Length 17;
Best Local Similarity 73.3%; Pred. No. 0.0046;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSI 15
   |||||:|||||
Db 2 CRVTHPLPKDIVRSI 16

RESULT 5
US-10-325-375A-6
; Sequence 6, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krah, Eugene R.
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of IgE to a High
; TITLE OF INVENTION: Affinity Receptor
; FILE REFERENCE: MBHB-01-672-E
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to IgE.
US-10-325-375A-6

Query Match          47.8%; Score 65; DB 15; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.017;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSI 16
   |||||:|||||
Db 2 CRVTHPLPKDIVRSI 17

RESULT 6
US-10-325-375A-5
; Sequence 5, Application US/10325375A
; Publication No. US20030229021A1
; GENERAL INFORMATION:
; APPLICANT: IDEXX Laboratories, Inc.
; APPLICANT: Krah, Eugene R.
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Methods and Compositions for Inhibiting Binding of IgE to a High
; TITLE OF INVENTION: Affinity Receptor
; FILE REFERENCE: MBHB-01-672-E
; CURRENT APPLICATION NUMBER: US/10/325,375A
; CURRENT FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Isolated polypeptide that binds to IgE.
US-10-325-375A-5

Query Match          44.9%; Score 61; DB 15; Length 17;
Best Local Similarity 75.0%; Pred. No. 0.064;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIVRSI 16
   |||||:|||||
```



Db 2 CKVTHDPLVIVRSI 17

## RESULT 7

US-10-362-527-313  
; Sequence 313, Application US/10362527  
; Publication No. US20040030106A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Mason, Sean  
; APPLICANT: Turnell, William Gordon  
; APPLICANT: Vinals Y De Bassols, Carlota  
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies  
; FILE REFERENCE: B45236  
; CURRENT APPLICATION NUMBER: US/10/362,527  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/09576  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: GB 0020717.5  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 313  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial variant of Homo sapiens IgE peptide  
US-10-362-527-313

Query Match 44.1%; Score 60; DB 12; Length 14;  
Best Local Similarity 69.2%; Pred. No. 0.072;  
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIV 13

Db 1 CRVTHPLPALM 13

## RESULT 8

US-10-304-443-107  
; Sequence 107, Application US/10304443  
; Publication No. US20030170229A1  
; GENERAL INFORMATION:  
; APPLICANT: Smithline Beecham Biologicals s.a.  
; APPLICANT: Peptide Therapeutics Ltd.  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45173CIP  
; CURRENT APPLICATION NUMBER: US/10/304,443  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: US/09/698,906A  
; PRIOR FILING DATE: 2001-02-20  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 107  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Human peptide sequence  
US-10-304-443-107

Query Match 44.1%; Score 60; DB 14; Length 14;  
Best Local Similarity 69.2%; Pred. No. 0.072;  
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIV 13

Db 1 CRVTHPLPALM 13

## RESULT 9

US-10-304-443-97  
; Sequence 97, Application US/10304443

; Publication No. US20030170229A1  
; GENERAL INFORMATION:  
; APPLICANT: Smithline Beecham Biologicals s.a.  
; APPLICANT: Peptide Therapeutics Ltd.  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45173CIP  
; CURRENT APPLICATION NUMBER: US/10/304,443  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: US/09/698,906A  
; PRIOR FILING DATE: 2001-02-20  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 97  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Human peptide sequence  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: (2)  
; OTHER INFORMATION: Where Xaa represents any 1 of 20 naturally occurring amino acids  
US-10-304-443-97

Query Match 44.1%; Score 60; DB 14; Length 16;  
Best Local Similarity 71.4%; Pred. No. 0.084;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPLPKDIVRS 15

Db 3 RVTHPLPALMRS 16

## RESULT 10

US-10-304-443-120  
; Sequence 120, Application US/10304443  
; Publication No. US20030170229A1  
; GENERAL INFORMATION:  
; APPLICANT: Smithline Beecham Biologicals s.a.  
; APPLICANT: Peptide Therapeutics Ltd.  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45173CIP  
; CURRENT APPLICATION NUMBER: US/10/304,443  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: US/09/698,906A  
; PRIOR FILING DATE: 2001-02-20  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 120  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Human peptide sequence  
US-10-304-443-120

Query Match 44.1%; Score 60; DB 14; Length 16;  
Best Local Similarity 71.4%; Pred. No. 0.084;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPLPKDIVRS 15

Db 3 RVTHPLPALMRS 16

## RESULT 11

US-10-362-527-315  
; Sequence 315, Application US/10362527  
; Publication No. US20040030106A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Mason, Sean  
; APPLICANT: Turnell, William Gordon  
; APPLICANT: Vinals Y De Bassols, Carlota  
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies  
; FILE REFERENCE: B45236

; CURRENT APPLICATION NUMBER: US/10/362,527  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/09576  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: GB 0020717.5  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 315  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial variant of Homo sapiens IgE peptide  
; NAME/KEY: VARIANT  
; LOCATION: (1)...(18)  
; OTHER INFORMATION: Xaa = Any Amino Acid  
US-10-362-527-315

Query Match 44.1%; Score 60; DB 12; Length 18;  
Best Local Similarity 71.4%; Pred. No. 0.095; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRS 15  
||| ||||| : : ||  
Db 4 RVTHPHLPALMRS 17

RESULT 12  
US-10-362-527-321  
; Sequence 321, Application US/10362527  
; Publication No. US2004030106A1  
; GENERAL INFORMATION:  
; APPLICANT: Friede, Martin  
; APPLICANT: Mason, Sean  
; APPLICANT: Turnell, William Gordon  
; APPLICANT: Vinals Y De Bassols, Carlota  
; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide  
; TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies  
; FILE REFERENCE: B45236  
; CURRENT APPLICATION NUMBER: US/10/362,527  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/EP01/09576  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: GB 0020717.5  
; PRIOR FILING DATE: 2000-08-22  
; NUMBER OF SEQ ID NOS: 328  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 321  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial variant of Homo sapiens IgE peptide  
US-10-362-527-321

Query Match 44.1%; Score 60; DB 12; Length 18;  
Best Local Similarity 71.4%; Pred. No. 0.095; 1; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRS 15  
||| ||||| : : ||  
Db 4 RVTHPHLPALMRS 17

RESULT 13  
US-10-304-443-98  
; Sequence 98, Application US/10304443  
; Publication No. US20030170229A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Biologicals s.a.  
; APPLICANT: Peptide Therapeutics Ltd.

; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45173CIP  
; CURRENT APPLICATION NUMBER: US/10/304,443  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: US/09/698,906A  
; PRIOR FILING DATE: 2001-02-20  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 98  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Human peptide sequence  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: (3)  
; OTHER INFORMATION: Where Xaa represents any 1 of 20 naturally occurring amino acids  
US-10-304-443-98

Query Match 44.1%; Score 60; DB 14; Length 18;  
Best Local Similarity 71.4%; Pred. No. 0.095; 3; Mismatches 1; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRS 15  
||| ||||| : : ||  
Db 4 RVTHPHLPALMRS 17

RESULT 14  
US-10-304-443-109  
; Sequence 109, Application US/10304443  
; Publication No. US20030170229A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Biologicals s.a.  
; APPLICANT: Peptide Therapeutics Ltd.  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45173CIP  
; CURRENT APPLICATION NUMBER: US/10/304,443  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: US/09/698,906A  
; PRIOR FILING DATE: 2001-02-20  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 109  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Human peptide sequence  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: (3)  
; OTHER INFORMATION: Where Xaa represents any 1 of 20 naturally occurring amino acids  
US-10-304-443-109

Query Match 44.1%; Score 60; DB 14; Length 18;  
Best Local Similarity 71.4%; Pred. No. 0.095; 3; Mismatches 1; Indels 0; Gaps 0;  
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRS 15  
||| ||||| : : ||  
Db 4 RVTHPHLPALMRS 17

RESULT 15  
US-10-304-443-115  
; Sequence 115, Application US/10304443  
; Publication No. US20030170229A1  
; GENERAL INFORMATION:  
; APPLICANT: SmithKline Beecham Biologicals s.a.  
; APPLICANT: Peptide Therapeutics Ltd.  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45173CIP  
; CURRENT APPLICATION NUMBER: US/10/304,443  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: US/09/698,906A

```

; PRIOR FILING DATE: 2001-02-20
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 115
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Human peptide sequence
US-10-304-443-115

Query Match      44.1%; Score 60; DB 14; Length 18;
Best Local Similarity 71.4%; Pred. No. 0.095;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      2 RVTHPHLPKDIVRS 15
Db      4 RVTHPHLPKDIVRS 17

Search completed: March 18, 2004, 14:07:04
Job time : 39 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:59:24 ; Search time 23 Seconds  
(without alignments)  
56.115 Million cell updates/sec

Title: US-09-938-700-4

Perfect score: 136

Sequence: 1 CRVTHPLPKDIVRSIAKPGKRAP 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 191815

Minimum DB seq length: 0

Maximum DB seq length: 25

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/2/iaa/5A COMB.pap.\*
  - 2: /cgn2\_6/ptodata/2/iaa/5B COMB.pap.\*
  - 3: /cgn2\_6/ptodata/2/iaa/6A COMB.pap.\*
  - 4: /cgn2\_6/ptodata/2/iaa/6B COMB.pap.\*
  - 5: /cgn2\_6/ptodata/2/iaa/PCTUS COMB.pap.\*
  - 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	47.1	25	3	US-09-100-414B-95
2	64	47.1	25	3	Sequence 95, Appl
3	64	47.1	25	4	US-09-303-323-95
4	60	44.1	22	4	Sequence 95, Appl
5	60	44.1	22	2	US-08-770-014-95
6	36	26.5	18	2	US-08-232-539D-19
7	36	26.5	22	2	Sequence 19, Appl
8	36	26.5	22	2	US-08-232-539D-20
9	35.5	26.1	22	1	Sequence 20, Appl
10	35.5	26.1	22	2	US-09-017-205-52
11	35	25.7	22	3	Sequence 52, Appl
12	35	25.7	22	3	Sequence 18, Appl
13	35	25.7	22	3	Sequence 14, Appl
14	35	25.7	22	3	US-08-455-079-18
15	35	25.7	22	3	Sequence 12, Appl
16	35	25.7	22	3	US-08-455-079-14
17	35	25.7	22	3	US-08-455-079-18
18	35	25.7	22	3	US-08-455-079-14
19	34	25.0	21	2	US-07-988-925-12
20	34	25.0	21	2	US-08-780-780-12
21	34	25.0	21	2	US-08-780-780-12
22	34	25.0	21	2	US-08-780-780-12
23	34	25.0	21	2	US-08-780-780-12
24	34	25.0	21	2	US-08-780-780-12
25	34	25.0	21	2	US-08-780-780-12
26	34	25.0	21	2	US-08-780-780-12
27	34	25.0	21	2	US-08-780-780-12

28	32	23.5	24	4	US-08-842-322-9	Sequence 9, Appl
29	32	23.5	24	4	US-09-316-919-31	Sequence 31, Appl
30	31.5	23.2	15	2	US-08-934-222-87	Sequence 87, Appl
31	31.5	23.2	15	2	US-08-933-402-87	Sequence 87, Appl
32	31.5	23.2	15	2	US-09-207-621-87	Sequence 87, Appl
33	31.5	23.2	15	2	US-08-532-818-87	Sequence 87, Appl
34	31.5	23.2	15	3	US-09-231-797-87	Sequence 87, Appl
35	31.5	23.2	15	3	US-08-934-224-87	Sequence 87, Appl
36	31.5	23.2	15	3	US-08-933-843-87	Sequence 87, Appl
37	31.5	23.2	15	3	US-08-934-223-87	Sequence 87, Appl
38	31.5	23.2	15	3	US-09-413-492-87	Sequence 103, App
39	31	22.8	14	5	PCT-US93-06751-103	Sequence 5, Appl
40	31	22.8	15	2	US-08-455-079-5	Sequence 9, Appl
41	31	22.8	22	1	US-08-148-209A-9	Sequence 21, Appl
42	31	22.8	24	3	US-08-592-500-27	Sequence 27, Appl
43	31	22.8	24	3	US-08-195-006-27	Sequence 27, Appl
44	31	22.8	24	5	PCT-US94-07644A-27	Sequence 37, Appl
45	30.5	22.4	18	4	US-09-390-134B-37	

## ALIGNMENTS

RESULT 1  
US-09-100-414B-95  
; Sequence 95, Application US/09100414B  
; Patent No. 6025468  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Chang Yi  
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE  
; TITLE OF INVENTION: IMMUNOGENS  
; NUMBER OF SEQUENCES: 106  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morgan & Finnegan, L.L.P.  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10154-0054  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC Windows  
; SOFTWARE: Word 97  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/100,414B  
; FILING DATE: 20-JUNE-1998  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Maria H. Lin  
; REGISTRATION NUMBER: 29,323  
; REFERENCE/DOCKET NUMBER: 1151-4157  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-758-4800  
; TELEFAX: 212-751-6849  
; INFORMATION FOR SEQ ID NO: 95:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 25 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-100-414B-95

Query Match 47.1%; Score 64; DB 3; Length 25;  
Best Local Similarity 64.7%; Pred. No. 0.002;  
Matches 11; Conservative 3; Mismatches 0; Gaps 0;  
Qy 2 RVTHPLPKDIVRSIAK 18  
Db 8 RVTHPLPKALMRSTTK 24  
RESULT 2

```
US-09-303-323-95
; Sequence 95, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-751-6840
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-303-323-95

Query Match 47.1%; Score 64; DB 3; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.002;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPLPKDIVRSIAK 18
| | | | | | | | | | | | | | | | | | | | |
Db 8 RVTHPLPALMRSTTK 24

RESULT 3
US-09-770-014-95
; Sequence 95, Application US/09770014
; Patent No. 6559282
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: IMMUNOGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/770,014
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

Query Match 47.1%; Score 64; DB 4; Length 25;
Best Local Similarity 64.7%; Pred. No. 0.002;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPLPKDIVRSIAK 18
| | | | | | | | | | | | | | | | | | | | |
Db 8 RVTHPLPALMRSTTK 24

RESULT 4
US-08-232-539D-19
; Sequence 19, Application US/08232539D
; Patent No. 5965709
; GENERAL INFORMATION:
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardiou, Paula M.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,539D
; FILING DATE: 21-APR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/178583
; FILING DATE: 07-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
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US-08-232-539D-19

Query Match 44.1%; Score 60; DB 2; Length 22;  
 Best Local Similarity 69.2%; Pred. No. 0.0075;  
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIV 13  
 |||||: :  
 Db 10 CRVTHPLPALM 22

RESULT 5

US-08-232-539D-20  
 ; Sequence 20, Application US/08232539D  
 ; Patent No. 5965709  
 ; GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.  
 APPLICANT: Jardieu, Paula M.  
 TITLE OF INVENTION: I9E Antagonists  
 NUMBER OF SEQUENCES: 60  
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/232,539D  
 FILING DATE: 21-Apr-1994  
 CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/178583  
 FILING DATE: 07-JAN-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/744768  
 FILING DATE: 14-AUG-1991  
 ATTORNEY/AGENT INFORMATION:

NAME: Svoboda, Craig G.  
 REGISTRATION NUMBER: 39,044  
 REFERENCE/DOCKET NUMBER: P0710P3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/952-1489  
 TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 24 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear

US-08-232-539D-20

Query Match 44.1%; Score 60; DB 2; Length 24;  
 Best Local Similarity 69.2%; Pred. No. 0.0083;  
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPLPKDIV 13  
 |||||: :  
 Db 12 CRVTHPLPALM 24

RESULT 6

US-09-017-205-52

; Sequence 52, Application US/09017205  
 ; Patent No. 5965357  
 ; GENERAL INFORMATION:

APPLICANT: Malsden, Howard S

TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN  
 DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2

NUMBER OF SEQUENCES: 86  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Nixon & Vanderhye PC  
 STREET: 8th Floor, 1100 No. 5965357th Glebe Road  
 CITY: Arlington  
 STATE: Virginia  
 COUNTRY: USA  
 ZIP: 22201-4714

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/017,205  
 FILING DATE: 02-FEB-1998

CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:

NAME: Mitchard, Leonard C  
 REGISTRATION NUMBER: 29,009  
 REFERENCE/DOCKET NUMBER: 604-436

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (703)816-4000  
 TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 52:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 amino acids  
 TYPE: amino acid

TOPOLOGY: linear  
 MOLECULE TYPE: peptide from HSV-2 glycoprotein G  
 FRAGMENT TYPE: internal  
 US-09-017-205-52

Query Match 26.5%; Score 36; DB 2; Length 18;  
 Best Local Similarity 75.0%; Pred. No. 35;  
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 THPHLPKD 11  
 |||||  
 Db 7 THPHGPAD 14

RESULT 7

US-08-455-079-18  
 ; Sequence 18, Application US/08455079  
 ; Patent No. 5994292  
 ; GENERAL INFORMATION:

APPLICANT: Tosato, Giovanna;  
 APPLICANT: Angiolillo, Anne L.; Sgadari, Cecilia  
 TITLE OF INVENTION: INTERFERON-INDUCIBLE  
 TITLE OF INVENTION: PROTEIN 10 IS A POTENT INHIBITOR OF  
 TITLE OF INVENTION: ANGIOGENESIS  
 NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORGAN & FINNEGAN, L.L.P.  
 STREET: 345 PARK AVENUE  
 CITY: NEW YORK  
 STATE: NEW YORK  
 COUNTRY: USA  
 ZIP: 10154

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5-INCH, 1.44 MB STORAGE  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,079  
 FILING DATE: 31-MAY-1995  
 ATTORNEY/AGENT INFORMATION:

NAME: KATHRYN M. BROWN  
 REGISTRATION NUMBER: 34,556  
 REFERENCE/DOCKET NUMBER: 2026-4182  
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 22 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
US-08-455-079-18

Query Match 26.5%; Score 36; DB 2; Length 22;  
Best Local Similarity 31.2%; Pred. No. 44;  
Matches 5: Conservative 8; Mismatches 3; Indels

```

RESULT 8
US-08-455-079-14
; Sequence 14, Application US/08455079
; Patent No. 5994292
; GENERAL INFORMATION:
; APPLICANT: Tosato, Giovanna;
; APPLICANT: Angiolillo, Anne L.; Sgadari, Cecilia
; TITLE OF INVENTION: INTERFERON-INDUCIBLE
; TITLE OF INVENTION: PROTEIN 10 IS A POTENT INHIBITOR OF
; TITLE OF INVENTION: ANGIOGENESIS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154

```

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5-INCH, 1.44 MB STORAGE  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WORDPERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,079  
FILING DATE: 31-MAY-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: KATHRYN M. BROWN  
REGISTRATION NUMBER: 34,556  
REFERENCE/DOCKET NUMBER: 2026-4182  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
TELEX: 421792  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
US-08-455-079-14

Query Match	26.5%;	Score 36;	DB 2;	Length 23;
Best Local Similarity	31.2%;	Pred. No. 46;		
Matches	5;	Conservative	8;	Mismatches 3;
				Indels

RESULT 9  
US-07-988-925-12

```

1  ; Sequence 12, Application US/07988925
2  ; Patent No. 5585097
3  ; GENERAL INFORMATION:
4  ; APPLICANT: Bolt, Sarah L
5  ; APPLICANT: Clark, Michael R
6  ; APPLICANT: Gorman, Scott D
7  ; APPLICANT: Routledge, Edward G
8  ; APPLICANT: Waldmann, Hermar
9  ; TITLE OF INVENTION: antibody preparation
10 ; NUMBER OF SEQUENCES: 24
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESSEE: Nixon and Vandethye pc
13 ; STREET: 11th Floor, 1100 No. 5585097th Glebe Road
14 ; CITY: Arlington
15 ; STATE: Virginia
16 ; COUNTRY: USA
17 ; ZIP: 22201
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: US/07/988,925
25 ; FILING DATE:
26 ; CLASSIFICATION: 424
27 ; PRIOR APPLICATION DATA:
28 ; APPLICATION NUMBER: GB 9206422.9
29 ; FILING DATE: 24-MAR-1992
30 ; PRIOR APPLICATION DATA:
31 ; APPLICATION NUMBER: WO PCT/GB92/01933
32 ; FILING DATE: 21-OCT-1992
33 ; ATTORNEY/AGENT INFORMATION:
34 ; NAME: Mitchard, Leonard C
35 ; REGISTRATION NUMBER: 29009
36 ; TELECOMMUNICATION INFORMATION:
37 ; TELEPHONE: 7038164000
38 ; TELEFAX: 7038164100
39 ; INFORMATION FOR SEQ ID NO: 12:
40 ; SEQUENCE CHARACTERISTICS:
41 ; LENGTH: 22 amino acids
42 ; TYPE: amino acid
43 ; STRANDEDNESS: single
44 ; TOPOLOGY: linear
45 ; MOLECULE TYPE: peptide
46 ;
47 ; US-07-988-925-12

```

Query Match 26.1%; Score 35.5; DB 1; Length 22;  
Best Local Similarity 35.0%; Pred. No. 52;  
Matches 7; Conservative 5; Mismatches 1; Indels

```

RESULT 10
US-08-362-780-12
: Sequence 12, Application US/08362780
: Patent No. 5968509
: GENERAL INFORMATION:
: APPLICANT: Gorman, Scott D
: APPLICANT: Routledge, Edward G
: APPLICANT: Waldmann, Herman
: TITLE OF INVENTION: Antibody Pre
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nixon and Vanderhve
: STREET: 8th Floor, 1100 No. 59
: CITY: Arlington
: STATE: Virginia
: COUNTRY: USA
: ZIP: 22201

```

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/362,780
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/862,543
; FILING DATE: 23-JUNE-1992
; APPLICATION NUMBER: GB 9021679.7
; FILING DATE: 05-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB91/01726
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mitchard, Leonard C
; REGISTRATION NUMBER: 29009
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-362-780-12

Query Match 26.1%; Score 35.5; DB 2; Length 22;
Best Local Similarity 35.0%; Pred. No. 52;
Matches 7; Conservative 5; Mismatches 1; Indels 7; Gaps 1;

Qy 3 VTHPLPKDIVRSIAKPGK 22
Db :||| |:::|||
4 LTQPH-----SVSESPGK 16

RESULT 11
US-09-046-985-4
; Sequence 4, Application US/09046985
; Patent No. 6121236
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: NOVEL MULTIVALENT LIGANDS WHICH MODULATE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/046,985
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,985
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= modified aa
; REFERENCE/DOCKET NUMBER: CMCC-614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; Query Match 25.7%; Score 35; DB 3; Length 22;
```

```
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= modified aa
; US-09-046-985-4

Query Match 25.7%; Score 35; DB 3; Length 22;
Best Local Similarity 40.0%; Pred. No. 63;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 HLPKDIVRSIAKPG 21
Db ||||: :|||
8 HRPKDYLSIVRRADG 22

RESULT 12
US-09-474-743-4
; Sequence 4, Application US/09474743
; Patent No. 6235716
; GENERAL INFORMATION:
; APPLICANT: Ben-Sasson, Shmuel A.
; TITLE OF INVENTION: NOVEL MULTIVALENT LIGANDS WHICH MODULATE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/474,743
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,985
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: CMCC-614
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781) 861-6240
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /label= modified aa
; US-09-474-743-4

Query Match 25.7%; Score 35; DB 3; Length 22;
```



Best Local Similarity 40.0%; Pred. No. 63;  
Matches 6; Conservative 3; Mismatches

6; Indels 0; Gaps 0;

QY 7 HLPKDIVRSIAKPG 21  
DB 8 HRPKOLSVIRRADG 22

RESULT 13  
US-08-851-843A-208  
; Sequence 208, Application US/08851843A  
; Patent No. 6093809  
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: No. 6093809el Telomerase  
NUMBER OF SEQUENCES: 225  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: United States of America  
ZIP: 94111

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,843A  
FILING DATE: 06-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002930US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 208:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

US-08-851-843A-208

Query Match 25.7%; Score 35; DB 3; Length 23;  
Best Local Similarity 38.5%; Pred. No. 66;  
Matches 10; Conservative 1; Mismatches 3; Indels 12; Gaps 2;

QY 4 THPH---LPKDIVRSIAKPGKRAP 25  
DB 6 TSPHPRENLPQD-----FGPRCP 23

## RESULT 14

US-08-974-549A-327  
; Sequence 327, Application US/08974549A  
; Patent No. 6166178  
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.  
APPLICANT: Lingner, Joachim  
APPLICANT: Nakamura, Toru  
APPLICANT: Chapman, Karen B.  
APPLICANT: Morin, Gregg B.  
APPLICANT: Harley, Calvin B.  
APPLICANT: Andrews, William H.  
TITLE OF INVENTION: Human Telomerase Catalytic Subunit  
NUMBER OF SEQUENCES: 727  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,549A  
FILING DATE: 19-NOV-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/724,643  
FILING DATE: 01-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/844,419  
FILING DATE: 18-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/846,017  
FILING DATE: 25-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,843  
FILING DATE: 06-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/854,050  
FILING DATE: 09-MAY-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/911,312  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/912,951  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/915,503  
FILING DATE: 14-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17618  
FILING DATE: 01-OCT-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/17885  
FILING DATE: 01-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph Ted  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 015389-002610US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 327:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 23 amino acids  
TYPE: amino acid

```
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-549A-327
Query Match      25.7%; Score 35; DB 3; Length 23;
Best Local Similarity 38.5%; Pred. No. 66;
Matches 10; Conservative 1; Mismatches 3; Indels 12; Gaps 2;

QY  4 THPH----LPKDIVRSIAKAPGKRAP 25
    |||||
Db   6 TSPHPRENLPQD-----PGPRCP 23

RESULT 15
US-08-854-050-208
; Sequence 208, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
```

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; MOLECULE TYPE: peptide
US-08-854-050-208
Query Match      25.7%; Score 35; DB 3; Length 23;
Best Local Similarity 38.5%; Pred. No. 66;
Matches 10; Conservative 1; Mismatches 3; Indels 12; Gaps 2;

QY  4 THPH----LPKDIVRSIAKAPGKRAP 25
    |||||
Db   6 TSPHPRENLPQD-----PGPRCP 23

Search completed: March 18, 2004, 14:02:44
Job time : 24 secs
```

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 18, 2004, 13:53:59 ; Search time 53 Seconds  
(without alignments)  
133.277 Million cell u

Title: US-09-938-700-4

Perfect score:

Sequence: 1 CRVTHPLPKDIVRSIAKAPGKRAP 25

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 546957

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Minimum DB seq length: 0
Maximum DB seq length: 25
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : A_Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003a.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
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## SUMMARIES

Result No.	Query \$			Description		
	Score	Match	Length	ID		
1	102	75.0	20	AAW24102	AAW24102	Canine im
2	89	65.4	17	AAW50894	AAW50894	Antibody
3	89	65.4	17	AAW50893	AAW50893	Antibody
4	89	65.4	25	AAW79999	AAW79999	Optimised
5	79	58.1	20	AAW24103	AAW24103	Canine im
6	72	52.9	17	AAW50896	AAW50896	Antibody
7	69	50.7	17	AAW50895	AAW50895	Antibody
8	68	50.0	25	AAW80000	AAW80000	Optimised
9	65	47.8	17	AAW50898	AAW50898	Antibody
10	64	47.1	25	AAW68602	AAW68602	Peptide s
11	64	47.1	25	AAW91212	AAW91212	Modified
12	64	47.1	25	AAW79998	AAW79998	Optimised
13	63	46.3	25	AAW80077	AAW80077	Optimised
14	61	44.9	17	AAW50897	AAW50897	Antibody
15	60	44.1	14	AAO18028	AAO18028	Human im
16	60	44.1	14	ABJ00529	ABJ00529	Human Ige
17	60	44.1	16	AAO18018	AAO18018	Human im
18	60	44.1	16	AAO18041	AAO18041	Human im
19	60	44.1	18	AAO18030	AAO18030	Human im
20	60	44.1	18	AAO18019	AAO18019	Human im
21	60	44.1	18	AAO18042	AAO18042	Human im
22	60	44.1	18	AAO18036	AAO18036	Human im
23	60	44.1	18	ABJ00531	ABJ00531	Human Ige
24	60	44.1	20	ABJ00537	ABJ00537	Human Ige
25	60	44.1	20	AAO18031	AAO18031	Human im

## ALIGNMENTS

## RESULT 1

AAW24102	
ID.	AAW24102 standard; peptide; 20 AA.
XX	
XX	
XX	AAW24102;
DT	21-NOV-1997 (first entry)
XX	
DE	Canine immunoglobulin E peptide 5.
XX	
KW	Immunoglobulin E; IgE; anti-canine IgE
XX	
XX	Canis familiaris.
OS	
XX	
PN	JP09169795-A.
XX	
PD	30-JUN-1997.

Canine immunoglobulin E peptide fragment and related DNA - useful for the preparation of anti-canine immunoglobulin E antibody.

PS Claim 2: Page 9: 12pp: Japanese.

AAW24098-106 are peptide fragments containing at least 5 continuous amino acids of the partial canine immunoglobulin E (IgE) protein shown in AAW24097. The peptides are used for the preparation of anti-canine IgE antibody. The anti-canine IgE antibody can be used for the diagnosis of canine allergies

Sequence 20 AA:

Query Match	75.0%;	Score 102;	DB 2;	Length 20;
Best Local Similarity	100.0%;	Pred. No.	1.3e-08;	

QY 1 CRVTHPLPKDIVRSIAKA 19  
|||  
db 2 CRVTHPLPKDIVRSIAKA 20  
|||

```

RESULT 2
AAV50894
ID AAY50894 standard; peptide; 17 AA.
XX AC AAY50894;
XX DT 24-FEB-2000 (first entry)
XX DE Antobody 15A.2 canine IgE binding epitope 1.
XX KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
XX KW epitope; prophylaxis; treatment; mimotope.
XX OS Synthetic.
XX PN EP957111-A2.
XX PD 17-NOV-1999.
XX PF 09-APR-1999; 99EP-00107035.
XX PR 09-APR-1998; 98US-00058331.
XX PR 30-MAR-1999; 99US-00281760.
XX PA (IDEX-) IDEXX LAB INC.
XX PI Lawton R, Mermer B, Francoeur G;
XX DR WPI; 2000-040833/04.
XX PT Binding proteins used for treatment or prophylaxis of canine allergy.
XX PS Disclosure; Fig 7; 30pp; English.
XX CC This invention describes a novel binding protein which specifically binds
CC to native canine free or B-cell bound IgE, and which doesn't bind to IgE
CC when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy. AAY50876-
CC Y50900 represent peptide mimotopes used in the method of the invention
XX SQ Sequence 17 AA;
PI Lawton R, Mermer B, Francoeur G;
XX DR WPI; 2000-040833/04.
XX PT Binding proteins used for treatment or prophylaxis of canine allergy.
XX PS Disclosure; Fig 7; 30pp; English.
XX CC This invention describes a novel binding protein which specifically binds
CC to native canine free or B-cell bound IgE, and which doesn't bind to IgE
CC when the IgE is bound to mast cells. The peptide products of the
CC invention have anti-allergic activity. The antibodies bind to defined
CC epitopes on free or B-cell bound IgE molecules which have an important
CC role in allergic reaction. The specific binding proteins are used to
CC produce a pharmaceutical composition, preferably with a diluent, which
CC can be used for prophylaxis or treatment of canine allergy. AAY50876-
CC Y50900 represent peptide mimotopes used in the method of the invention
XX SQ Sequence 17 AA;
Query Match 65.4%; Score 89; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRVTHPLPKDIVRSI 16
Db 2 CRVTHPLPKDIVRSI 17
RESULT 3
AAV50893
ID AAY50893 standard; peptide; 17 AA.
XX AC AAY50893;
XX DT 24-FEB-2000 (first entry)
XX DE Antobody 15A.2 binding peptide 10 from PhDc7c phage display library.
XX KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;
XX KW epitope; prophylaxis; treatment; mimotope.
XX OS Synthetic.
XX PN EP957111-A2.
XX PD 17-NOV-1999.
XX PF 09-APR-1999; 99EP-00107035.
XX PR 09-APR-1998; 98US-00058331.
XX PR 30-MAR-1999; 99US-00281760.
XX PA (IDEX-) IDEXX LAB INC.
XX PI Lawton R, Mermer B, Francoeur G;
XX DR WPI; 2000-040833/04.
XX PT Binding proteins used for treatment or prophylaxis of canine allergy.
XX PS Disclosure; Fig 7; 30pp; English.
XX CC This invention describes a novel binding protein which specifically binds
XX to native canine free or B-cell bound IgE, and which doesn't bind to IgE
XX when the IgE is bound to mast cells. The peptide products of the
XX invention have anti-allergic activity. The antibodies bind to defined
XX epitopes on free or B-cell bound IgE molecules which have an important
XX role in allergic reaction. The specific binding proteins are used to
XX produce a pharmaceutical composition, preferably with a diluent, which
XX can be used for prophylaxis or treatment of canine allergy. AAY50876-
XX Y50900 represent peptide mimotopes used in the method of the invention
XX SQ Sequence 17 AA;
Query Match 65.4%; Score 89; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRVTHPLPKDIVRSI 16
Db 2 CRVTHPLPKDIVRSI 17
RESULT 4
AAV79999
ID AAY79999 standard; peptide; 25 AA.
XX AC AAY79999;
XX DT 15-MAY-2000 (first entry)
XX DE Optimised IgE-CH3 domain antigen peptide for dog IgE.
XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
XX KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
XX KW antibody; allergy; allergic disease; immunisation; anti-allergic;
XX KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX OS Canis sp.
XX OS Synthetic.
XX PN WO9967293-A1.
XX PD 29-DEC-1999.
XX PF 21-JUN-1999; 99WO-US013959.
XX PR 20-JUN-1998; 98US-00100287.
XX PA (UNBI-) UNITED BIOMEDICAL INC.
XX PI Wang CY, Walfield AM;
XX PR WPI; 2000-160578/14.
XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX for immunization against allergy.

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PD 17-NOV-1999.
XX 09-APR-1999; 99EP-00107035.
XX 09-APR-1998; 98US-00058331.
XX 30-MAR-1999; 99US-00281760.
XX (IDEX-) IDEXX LAB INC.
XX Lawton R, Mermer B, Francoeur G;
XX WPI; 2000-040833/04.
XX Binding proteins used for treatment or prophylaxis of canine allergy.
XX Disclosure; Fig 6; 30pp; English.
XX This invention describes a novel binding protein which specifically binds
XX to native canine free or B-cell bound IgE, and which doesn't bind to IgE
XX when the IgE is bound to mast cells. The peptide products of the
XX invention have anti-allergic activity. The antibodies bind to defined
XX epitopes on free or B-cell bound IgE molecules which have an important
XX role in allergic reaction. The specific binding proteins are used to
XX produce a pharmaceutical composition, preferably with a diluent, which
XX can be used for prophylaxis or treatment of canine allergy. AAY50876-
XX Y50900 represent peptide mimotopes used in the method of the invention
XX SQ Sequence 17 AA;
Query Match 65.4%; Score 89; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CRVTHPLPKDIVRSI 16
Db 2 CRVTHPLPKDIVRSI 17
RESULT 4
AAV79999
ID AAY79999 standard; peptide; 25 AA.
XX AC AAY79999;
XX DT 15-MAY-2000 (first entry)
XX DE Optimised IgE-CH3 domain antigen peptide for dog IgE.
XX KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
XX KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
XX KW antibody; allergy; allergic disease; immunisation; anti-allergic;
XX KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
XX OS Canis sp.
XX OS Synthetic.
XX PN WO9967293-A1.
XX PD 29-DEC-1999.
XX PF 21-JUN-1999; 99WO-US013959.
XX PR 20-JUN-1998; 98US-00100287.
XX PA (UNBI-) UNITED BIOMEDICAL INC.
XX PI Wang CY, Walfield AM;
XX PR WPI; 2000-160578/14.
XX PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
XX for immunization against allergy.

```

PS Claim 1; Page 99; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain  
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and  
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for  
 CC a target effector site on the epsilon-heavy chain of IgE, and so  
 CC preventing triggering and activation of mast cells and basophils and  
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,  
 CC containing (I) are used for active immunisation against IgE-mediated  
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy  
 CC dermatitis. Nucleic acids that encode these compounds are useful for  
 CC recombinant production of corresponding peptides or in DNA vaccines.  
 CC Conjugates of (I) that include a promiscuous T helper cell epitope  
 CC (functional in genetically diverse subjects), in addition to a B cell  
 CC target epitope, have increased immunogenicity and may include cyclic  
 CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAY7994 to AAY8084 represent amino acid  
 CC sequences used in the exemplification of the present invention

XX Sequence 25 AA;

Query Match 65.4%; Score 89; DB 3; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18  
 DB 8 RVTHPHLPKDIVRSIAK 24  
 |||||

RESULT 5

AAW24103  
 ID AAW24103 standard; peptide; 20 AA.

XX AAW24103;

XX 21-NOV-1997 (first entry)

XX Canine immunoglobulin E peptide 6.

XX Immunoglobulin E; IgE; anti-canine IgE antibody; allergy; canine; dog.

XX Canis familiaris.

XX JP09169795-A.

XX 30-JUN-1997.

XX 22-DEC-1995; 95JP-00334381.

XX 22-DEC-1995; 95JP-00334381.

XX (HITB ) HITACHI CHEM CO LTD.

XX WPI; 1997-389423/36.

XX N-PSDB; AAT85652.

XX Canine immunoglobulin E peptide fragment and related DNA - useful for the  
 PT preparation of anti-canine immunoglobulin E antibody.

XX Claim 2; Page 9; 12pp; Japanese.

XX AAW24098-106 are peptide fragments containing at least 5 continuous amino  
 CC acids of the partial canine immunoglobulin E (IgE) protein shown in  
 CC AAW24097. The peptides are used for the preparation of anti-canine IgE  
 CC antibody. The anti-canine IgE antibody can be used for the diagnosis of  
 CC canine allergies

XX Sequence 20 AA;

Query Match 58.1%; Score 79; DB 2; Length 20;  
 Best Local Similarity 100.0%; Pred. No. 4.6e-05;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KDIVRSIAKAPGRAP 25  
 DB 1 KDIVRSIAKAPGRAP 16  
 |||||

RESULT 6

AAV50896  
 ID AAV50896 standard; peptide; 17 AA.

XX AAV50896;

XX 24-FEB-2000 (first entry)

XX Antibody 15A.2 green monkey IgE binding epitope 1.

XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;  
 KW epitope; prophylaxis; treatment; mimotope.

XX Synthetic.

XX EP957111-A2.

XX 17-NOV-1999.

XX 09-APR-1999; 99EP-00107035.

XX 09-APR-1998; 98US-00058331.

XX 30-MAR-1999; 99US-00281760.

XX (IDEX-) IDEX LAB INC.

XX Lawton R, Mermer B, Francoeur G;

XX WPI; 2000-040833/04.

XX Binding proteins used for treatment or prophylaxis of canine allergy.

XX Disclosure; Fig 7; 30pp; English.

XX This invention describes a novel binding protein which specifically binds  
 CC to native canine free or B-cell bound IgE, and which doesn't bind to IgE  
 CC when the IgE is bound to mast cells. The peptide products of the  
 CC invention have anti-allergic activity. The antibodies bind to defined  
 CC epitopes on free or B-cell bound IgE molecules which have an important  
 CC role in allergic reaction. The specific binding proteins are used to  
 CC produce a pharmaceutical composition, preferably with a diluent, which  
 CC can be used for prophylaxis or treatment of canine allergy. AAY50876-  
 CC Y50900 represent peptide mimotopes used in the method of the invention

XX Sequence 17 AA;

Query Match 52.9%; Score 72; DB 3; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 0.00047;  
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRVTHPHLPKDIVRS 15  
 DB 2 CRVTHPHLPALVRS 16  
 |||||

RESULT 7

AAV50895  
 ID AAV50895 standard; peptide; 17 AA.

XX AAV50895;

XX 24-FEB-2000 (first entry)

XX Antibody 15A.2 human IgE binding epitope 1.

XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;

KW epitope; prophylaxis; treatment; mimotope.  
 XX  
 OS Synthetic.  
 XX EP957111-A2.  
 PN  
 XX  
 PD 17-NOV-1999.  
 XX  
 PF 09-APR-1999; 99EP-00107035.  
 XX  
 PR 09-APR-1998; 98US-00058331.  
 PR 30-MAR-1999; 99US-00281760.  
 XX  
 PA (IDEX-) IDEXX LAB INC.  
 XX  
 PI Lawton R, Mermer B, Francoeur G;  
 XX  
 DR WPI; 2000-040833/04.  
 XX  
 PT Binding proteins used for treatment or prophylaxis of canine allergy.  
 PS Disclosure; Fig 7; 30pp; English.  
 XX  
 CC This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE when the IgE is bound to mast cells. The peptide products of the invention have anti-allergic activity. The antibodies bind to defined epitopes on free or B-cell bound IgE molecules which have an important role in allergic reaction. The specific binding proteins are used to produce a pharmaceutical composition, preferably with a diluent, which can be used for prophylaxis or treatment of canine allergy. AAY50876-Y50900 represent peptide mimotopes used in the method of the invention  
 XX  
 SQ Sequence 17 AA;  
 Query Match 50.7%; Score 69; DB 3; Length 17;  
 Best Local Similarity 73.3%; Pred. No. 0.0014;  
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CRVTHPLPKDIVRS 15  
 DB 2 CRVTHPLPKDIVRS 16  
 RESULT 8  
 AAY80000  
 ID AAY80000 standard; peptide; 25 AA.  
 XX  
 AC AAY80000;  
 XX  
 DT 15-MAY-2000 (first entry)  
 XX  
 DE Optimised IgE-CH3 domain antigen peptide for rat IgE.  
 XX  
 KW Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;  
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;  
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;  
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.  
 XX  
 OS Rattus sp.  
 OS Synthetic.  
 XX  
 PN WO9967293-A1.  
 XX  
 PD 29-DEC-1999.  
 XX  
 PF 21-JUN-1999; 99WO-US013959.  
 XX  
 PR 20-JUN-1998; 98US-00100287.  
 XX  
 PA (UNBI-) UNITED BIOMEDICAL INC.  
 XX  
 PI Wang CY, Walfield AM;

XX WPI; 2000-160578/14.  
 DR  
 XX  
 PT New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.  
 XX  
 PS Claim 1; Page 99; 155pp; English.  
 XX  
 CC The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention  
 XX  
 SQ Sequence 25 AA;  
 Query Match 50.0%; Score 68; DB 3; Length 25;  
 Best Local Similarity 76.5%; Pred. No. 0.003;  
 Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 2 RVTHPLPKDIVRSIAK 18  
 DB 8 RVDRHPFKPIVRSITK 24  
 RESULT 9  
 AAY50898  
 ID AAY50898 standard; peptide; 17 AA.  
 XX  
 AC AAY50898;  
 XX  
 DT 24-FEB-2000 (first entry)  
 XX  
 DE Antibody 15A.2 swine IgE binding epitope 1.  
 XX  
 KW Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy; epitope; prophylaxis; treatment; mimotope.  
 XX  
 OS Synthetic.  
 XX  
 PN EP957111-A2.  
 XX  
 PD 17-NOV-1999.  
 XX  
 PF 09-APR-1999; 99EP-00107035.  
 XX  
 PR 09-APR-1998; 98US-00058331.  
 PR 30-MAR-1999; 99US-00281760.  
 XX  
 PA (IDEX-) IDEXX LAB INC.  
 XX  
 PI Lawton R, Mermer B, Francoeur G;  
 XX  
 DR WPI; 2000-040833/04.  
 XX  
 PT Binding proteins used for treatment or prophylaxis of canine allergy.  
 PS Disclosure; Fig 7; 30pp; English.  
 XX  
 CC This invention describes a novel binding protein which specifically binds to native canine free or B-cell bound IgE, and which doesn't bind to IgE

CC when the Ige is bound to mast cells. The peptide products of the  
 CC invention have anti-allergic activity. The antibodies bind to defined  
 CC epitopes on free or B-cell bound Ige molecules which have an important  
 CC role in allergic reaction. The specific binding proteins are used to  
 CC produce a pharmaceutical composition, preferably with a diluent, which  
 CC can be used for prophylaxis or treatment of canine allergy. AAY50876-  
 CC Y50900 represent peptide mimotopes used in the method of the invention  
 XX SQ Sequence 17 AA;

Query Match 47.8%; Score 65; DB 3; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 0.0057;  
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRVTHPLPKDIVRSI 16  
 | | | | | | | | | | | | | | | | | |  
 Db 2 CNVTHPLPKDIVRSI 17

RESULT 10  
 AAY68602  
 ID AAY68602 standard; peptide; 25 AA.  
 XX  
 AC AAY68602;  
 XX  
 DT 05-MAY-2000 (first entry)  
 XX  
 DE Peptide sequence of the invention.  
 XX  
 KW Helper T cell epitope; peptide immunogen; LHRH;  
 KW luteinizing hormone-releasing hormone; spermatogenesis; ovulation;  
 KW oestrus; sexual development; sex hormone; promiscuous T helper epitope;  
 KW vaccine; contraceptive; hormone-dependent tumour; prostate cancer;  
 KW breast cancer; endometriosis; boar taint; meat quality; immunocastration.  
 XX

OS Unidentified.

XX WO9966952-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013960.

XX 20-JUN-1998; 98US-00100414.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2000-160562/14.

XX New peptide immunogen containing luteinizing hormone-releasing hormone  
 PT antigen site and helper T cell epitope, for e.g. contraception and  
 PT treatment of cancer.

PS Disclosure; Page 92; 102pp; English.

CC The specification describes peptide immunogens comprising a synthetic  
 CC helper T cell (Th) epitope and a target antigen, luteinising hormone-  
 CC releasing hormone (LHRH). The peptide immunogens cause induction of a  
 CC specific immune response to LHRH which is involved in regulation of  
 CC spermatogenesis, ovulation, oestrus, sexual development and secretion of  
 CC sex hormones. Provision of a promiscuous T helper epitope (which is  
 CC functional in genetically diverse subjects) provides optimum  
 CC immunogenicity to the B cell epitopes of the target antigen and thus high  
 CC antibody titres against the target antigen. The peptide immunogens of the  
 CC invention are used to vaccinate against mammalian LHRH, for use as  
 CC (reversible) contraceptive; control of hormone-dependent tumours (cancer  
 CC of prostate or breast, also endometriosis); to prevent boar taint (and  
 CC improve meat quality) and for immunocastration. The present sequence  
 CC appears in the specification

XX SQ Sequence 25 AA;

Query Match 47.1%; Score 64; DB 3; Length 25;  
 Best Local Similarity 64.7%; Pred. No. 0.013;  
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RVTHPLPKDIVRSIAK 18  
 | | | | | | | | | | | | | | | | | |  
 Db 8 RVTHPLPALMRSTTK 24

RESULT 11  
 AAY91212  
 ID AAY91212 standard; peptide; 25 AA.  
 XX  
 AC AAY91212;  
 XX  
 DT 22-MAY-2000 (first entry)  
 XX  
 DE Modified human Ige CH3 domain, SEQ ID NO:92.

XX Promiscuous T-cell epitope; measles virus F protein; MVF;  
 KW hepatitis B virus surface antigen; HBV, immunogenic; B-cell epitope;  
 KW luteinising hormone releasing hormone; LHRH; contraceptive; anticancer;  
 KW somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV;  
 KW foot and mouth disease virus; immunoglobulin E; Ige; anti-allergic;  
 KW Plasmodium falciparum; circumsporozoite; antimalarial; CPTp;  
 KW cholesteryl ester transport protein; anti-arteriosclerotic.  
 XX

OS Homo sapiens.

OS Synthetic.

XX WO9966957-A2.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013975.

XX 20-JUN-1998; 98US-00100412.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY;

XX WPI; 2000-160564/14.

XX New artificial T helper cell epitope and derived immunogens with target  
 PT antigenic site, for immunization against e.g. malaria, arteriosclerosis  
 PT or human immune deficiency virus.

XX Example 6; Page 40; 129pp; English.

XX The invention relates to novel promiscuous T helper cell epitopes (Th),  
 CC and immunogenic peptides comprising the Th epitopes of the invention  
 CC along with B cell epitopes. The Th epitopes and peptide immunogens  
 CC containing them, are used to induce a T helper cell response,  
 CC specifically against Plasmodium falciparum, cholesteryl ester transport  
 CC protein (CPTp) or HIV epitopes, but more generally against any pathogen,  
 CC immunoreactive self-antigen or tumour antigen. The Th epitopes and  
 CC peptide immunogens may be used for prevention and/or treatment of  
 CC infections (HIV, foot-and-mouth disease or malaria); for cancer  
 CC immunotherapy; for inhibition of the action of luteinising hormone-  
 CC releasing hormone (LHRH) for contraception, treatment of hormone-  
 CC dependent cancer, prevention of boar taint in meat, and immunocastration)  
 CC ; for promoting the growth of animals; or for treating allergies or  
 CC arteriosclerosis. Incorporation of a promiscuous Th (functional in  
 CC genetically diverse subjects) into an immunogen improves capacity to  
 CC induce a strong T helper cell-mediated immune response, resulting in  
 CC production of antibodies against a target antigen. Th can replace carrier  
 CC proteins and pathogen-derived T helper epitopes. Sequence AAY91121  
 CC represents a promiscuous T helper epitope from the measles virus F (MVF)  
 CC protein and sequences AAY91122-Y91142, AAY91226 and AAY91245-Y91246  
 CC represent synthetic Th epitopes based on the MVF Th epitope. Sequence  
 CC AAY91143 represents a promiscuous Th epitope from hepatitis B virus (HBV)

CC surface antigen, and sequences AAY91144-Y91155 are synthetic epitopes  
 CC derived from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-  
 CC Y91244 are antigenic peptides comprising an LHRH sequence joined to a  
 CC promiscuous Th epitope. AAY91197 is the LHRH target antigenic peptide  
 CC used in these LHRH antigenic peptides. AAY91200 is somatostatin, and  
 CC AAY91201-Y91207 are antigenic peptides comprising somatostatin, and a Th  
 CC epitope. Somatostatin immunogens may be used to promote growth in  
 CC livestock. AAY91208 is a human CD4 CDR2-like domain antigenic site, and  
 CC AAY91209-Y90211 are MVH Th epitope/CD4 CDR2 antigenic peptides which may  
 CC be used to prevent HIV infection of T cells. AAY90212 is a modified  
 CC version of a human IgE (immunoglobulin E) CH3 domain, and AAY90213-Y90219  
 CC are Th epitope/IgE CH3 antigenic peptides which may be used in the  
 CC treatment of allergies. AAY91220 is a peptide derived from foot and mouth  
 CC disease virus (FMDV) VP1 capsid protein and AAY91221-Y91222 comprise this  
 CC peptide and a Th epitope. AAY91223 is a Plasmodium falciparum  
 CC circumsporozoite (CS) target antigen, and AAY91224-Y91225 comprise the CS  
 CC antigen and an MVF Th epitope and may be used in a malaria vaccine.  
 CC AAY91228-Y91231 represent CERP-derived peptides and AAY91232-Y91241 are  
 CC immunogens comprising a CERP peptide and a Th epitope which may be used  
 CC to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247  
 CC and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-  
 CC Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and  
 CC HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1  
 CC vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory  
 CC invasin protein epitope from Yersinia species, and hinge spacer peptide,  
 CC both of which may optionally be used in the antigenic peptides of the  
 CC invention

XX Sequence 25 AA;

Query Match 47.1%; Score 64; DB 3; Length 25;  
 Best Local Similarity 64.7%; Pred. No. 0.013;  
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18  
 |||||:::|  
 Db 8 RVTHPHLPALMRSTTK 24

RESULT 12

ID AAY79998 standard; peptide; 25 AA.

XX AC AAY79998;

XX 15-MAY-2000 (first entry)

XX Optimised IgE-CH3 domain antigen peptide for human IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;  
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;  
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;  
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Homo sapiens.

OS Synthetic.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013959.

XX 20-JUN-1998; 98US-00100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions  
 PT for immunization against allergy.

XX Claim 1; Page 21; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain  
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and  
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for  
 CC a target effector site on the epsilon-heavy chain of IgE, and so  
 CC preventing triggering and activation of mast cells and basophils and  
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,  
 CC containing (I) are used for active immunisation against IgE-mediated  
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy  
 CC dermatitis. Nucleic acids that encode these compounds are useful for  
 CC recombinant production of corresponding peptides or in DNA vaccines.  
 CC Conjugates of (I) that include a promiscuous T helper cell epitope  
 CC (functional in genetically diverse subjects), in addition to a B cell  
 CC target epitope, have increased immunogenicity and may include cyclic  
 CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid  
 CC sequences used in the exemplification of the present invention

XX Sequence 25 AA;

Query Match 47.1%; Score 64; DB 3; Length 25;  
 Best Local Similarity 64.7%; Pred. No. 0.013;  
 Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 RVTHPHLPKDIVRSIAK 18  
 |||||:::|  
 Db 8 RVTHPHLPALMRSTTK 24

RESULT 13

ID AAY80077 standard; peptide; 25 AA.

XX AC AAY80077;

XX 15-MAY-2000 (first entry)

XX Optimised IgE-CH3 domain antigen peptide for horse IgE.

XX Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;  
 KW immunogenic; immunostimulatory; carrier protein; helper T cell epitope;  
 KW antibody; allergy; allergic disease; immunisation; anti-allergic;  
 KW anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

XX Equus caballus.

OS Synthetic.

XX WO9967293-A1.

XX 29-DEC-1999.

XX 21-JUN-1999; 99WO-US013959.

XX 20-JUN-1998; 98US-00100287.

XX (UNBI-) UNITED BIOMEDICAL INC.

XX Wang CY, Walfield AM;

XX WPI; 2000-160578/14.

XX New antigenic peptide from the CH3 domain of immunoglobulin E, fusions  
 PT for immunization against allergy.

XX Claim 1; Page 146; 155pp; English.

XX The present invention describes immunoglobulin E (IgE)-CH3 domain  
 CC antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and  
 CC anti-asthmatic properties. (I) induces polyclonal antibodies specific for  
 CC a target effector site on the epsilon-heavy chain of IgE, and so



CC preventing triggering and activation of mast cells and basophils and  
 CC downregulation of IgE synthesis. Conjugates, or fusion peptides,  
 CC containing (I) are used for active immunisation against IgE-mediated  
 CC allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy  
 CC dermatitis. Nucleic acids that encode these compounds are useful for  
 CC recombinant production of corresponding peptides or in DNA vaccines.  
 CC Conjugates of (I) that include a promiscuous T helper cell epitope  
 CC (functional in genetically diverse subjects), in addition to a B cell  
 CC target epitope, have increased immunogenicity and may include cyclic  
 CC constraints (disulfide bridge) to stabilise conformational features and  
 CC maximize cross-reactivity to the natural target. They induce safe (non-  
 CC anaphylactogenic) antibodies. AAY7994 to AAY8084 represent amino acid  
 CC sequences used in the exemplification of the present invention

XX  
 SQ Sequence 25 AA;

Query Match 46.3%; Score 63; DB 3; Length 25;  
 Best Local Similarity 68.8%; Pred. No. 0.018; Indels 0; Gaps 0;  
 Matches 11; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VTHPHLPKDIVRSIAK 18  
 |::|::|::|::|::|  
 Db 9 VSHDPLPREVRSIAK 24

RESULT 14  
 AAY50897  
 ID AAY50897 standard; peptide; 17 AA.  
 AC AAY50897;  
 XX

DT 24-FEB-2000 (first entry)

DE Antibody 15A.2 feline IgE binding epitope 1.

XX Canine; allergy; antibody 15A.2; IgE; B cell; mast cell; anti-allergy;  
 KW epitope; prophylaxis; treatment; mimotope.

XX Synthetic.

XX EP957111-A2.

XX 17-NOV-1999.

XX 09-APR-1999; 99EP-00107035.

XX 09-APR-1998; 98US-00058331.

XX 30-MAR-1999; 99US-00281760.

XX (IDEX-) IDEX LAB INC.

XX Lawton R, Mermer B, Francoeur G;

XX WPI; 2000-040833/04.

XX Binding proteins used for treatment or prophylaxis of canine allergy.

XX Disclosure; Fig 7; 30pp; English.

XX This invention describes a novel binding protein which specifically binds  
 CC to native canine free or B-cell bound IgE, and which doesn't bind to IgE  
 CC when the IgE is bound to mast cells. The peptide products of the  
 CC invention have anti-allergic activity. The antibodies bind to defined  
 CC epitopes on free or B-cell bound IgE molecules which have an important  
 CC role in allergic reaction. The specific binding proteins are used to  
 CC produce a pharmaceutical composition, preferably with a diluent, which  
 CC can be used for prophylaxis or treatment of canine allergy. AAY50876-  
 CC Y50900 represent peptide mimotopes used in the method of the invention

XX Sequence 17 AA;

Query Match 44.9%; Score 61; DB 3; Length 17;  
 Best Local Similarity 75.0%; Pred. No. 0.024;

Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 Qy 1 CRVTHPHLPKDIVRSI 16  
 |::|::|::|::|::|  
 Db 2 CKVTHPDLPLVIVRSI 17

RESULT 15

AAO18028

ID AAO18028 standard; peptide; 14 AA.

XX AAO18028;

XX 30-AUG-2002 (first entry)

XX Human immunoglobulin E epitope SEQ ID NO: 20.

XX Allergy; immunoglobulin E; IgE; vaccine; immunogen; epitope; human;  
 KW non-anaphylactogenic; antiallergic.

XX Homo sapiens.

XX WO200234288-A2.

XX 02-MAY-2002.

XX 24-OCT-2001; 2001WO-EP012392.

XX 27-OCT-2000; 2000GB-00026334.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Vinals Y De BassolsC;

XX WPI; 2002-479702/51.

XX New peptides epitopes and mimotopes derived from IgE, useful for treating  
 PT or preventing allergies, for typing circulating anti-IgE, or for  
 PT diagnosing atopy.

XX Claim 1; Page 5; 28pp; English.

XX The present invention provides peptide epitopes derived from human  
 CC immunoglobulin E (IgE), which are non-anaphylactogenic and can be used as  
 CC immunogens to diagnose and treat allergies. The present sequence is an  
 CC epitope of the invention

XX Sequence 14 AA;

Query Match 44.1%; Score 60; DB 5; Length 14;

Best Local Similarity 69.2%; Pred. No. 0.027;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRVTHPHLPKDIV 13  
 |::|::|::|::|::|

Db 1 CRVTHPHLPALM 13

Search completed: March 18, 2004, 14:00:20

Job time : 54 secs